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length: 2000000000
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Match Length
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1: gb_ba:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

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REFERENCE AUTHORS TITLE JOURNAL KEYWORDS SOURCE ORGANISM ACCESSION VERSION RESULT 1
HS302D9
LOCUS
DEFINITION COMMENT Submitted (08-DEC-1999) sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 13, 1999 this sequence version replaced gi:3164067.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission Human DNA sequence from clone GSSs, complete sequence. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens Z82198 Z82198.2 GI:6572207 Bridgeman,A. Direct Submission ıuman (bases 1 to 145880) 145880 bp DNA linear PRI 12-DEC-199 om clone RP1-302D9 on chromosome 22 Contains PRI 12-DEC-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22 constructed by the Sanger Centre Chromosome 22 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known such as compressions and repeats, but not necessarily within known
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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2350...2
                                                                                                                                                                                                                                                      /note="14279...4
                                                                                                                                                  /note="AluJb repeat: 6369. .6485
                                                                                                                                                                                     /note="52 copies 2 mer ct 78 conserved"
5181. .5491
                                                                                                                                                                                                                     /note="MLT1E repeat: matches 359. 5073. .5176
                                                                                                                                                                                                                                                                                                                         3653
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3323. .3343
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572. .759
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246. .571
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/chromosome="22"
                                                                                                                                                                                                                                                                                                                                      3344. .3652
/note="Aluy repeat:
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                                 /note="MADE1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat: matches 2593.
                                                                                                                                  2 repeat:
repeat:
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matches 9.
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18296. .1832
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8414 .8551
/note="Lz repeat: matches 2553.
8914 .9030
                                                                                                                                /note="MLT1B repeat: 15728. .16027
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/note="""
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13398. 13598
/note="Alusp repeat: matches 1.
13699. 13810
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/note="MSTB repeat: matches 2.
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/note="MIR repeat:
13945. .14060
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/note="match: STS:
13331. .13397
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10784. .11201
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/note="FAM repeat: matches 3.
                                                                                                                                                                                                       /note="MLT1B repeat: matches l. 15490. .15662
                                                                                                                                                                                                                                                                                                                                           14616. .15060
                                                                                                                                                                                                                                                                                                                                                                                                            14589.
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14061. .14367
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10718. .11310
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/note="MIR repeat:
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15669. .15727
                                                                                                                                                                                                                                                                                                                                                                                                         /note="MIR repeat:
14589...14679
                                                                                                  /note="AluSc repeat: matches 1 . .299 of consensus"
16028 . .16245
                                                                                                                                                                                                                                                                                                                                                         note="match:
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                                                                                 note="MLT1B
                                                                                                                                                                                                                                                      'note="L2 repeat: matches 2112.
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.12642
                                                                                                                                                                                                                                                                      .15188
                                                                                                                                                                                                                                                                                                                                                                             .15201
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MSTA repeat: matches 2. .18392
                          .18323
                                                                   16854
                                                                                 repeat: matches 178.
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22302..22537
/note="MeR66-internal repeat: matches
consensus"
22538..22850
/note="Aluxp repeat: matches 1..313 o
22851..23801
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consensus"
18393 . 18712
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18713 . 19133
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consensus"
23905. .23989
/note="MER66-internal repeat:
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20513. .20666
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20317. .20382
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19537. .20290
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19251. .19719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.9%; Score 921; DB 9; 58.2%; Pred. No. 2e-211; tive 300; Mismatches 23
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                                                                                                GACTCCAGAAGGGTAGATCCACTGACAGCTTGCAGCATGTGCCTGAAAAATCCACAGACA
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     tyacncartgyytntayytncaytgyatg
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KEYWORDS SOURCE ACCESSION VERSION LOCUS DEFINITION RESULT AC025577 ORGANISM

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Homo sapiens BAC Library) AC025577 AC025577.15 AC025577 12 BAC RP complete 154090 bp DNA RP11-13C3 (Roswell sequence Park linear PRI 25-AUG-2000 Cancer Institute Human

REFERENCE AUTHORS Eukaryota; Mammalia; |

Homo sapiens

Craniata; Vertebrata;

Euteleostomi;

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밁

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 154090)

Muzny.D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J. Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R. Metazoa; Chordata; Eutheria; Primates; Barbaria, J.,

Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., Davida, R., Davida, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Garca, N., Gill, R., Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hartt, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Han, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Jacobson, B., Jia, Y., Hohnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L.C., Liu, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Lucier, R., Luna, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metker, M., Miller, A., Miner, G., Merscher, S., Metker, M., Miller, A., Miner, G., Meston, M., Nguyen, N., Nguyen, N., Nickerson, E., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pull, L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Shim, C., Shooshtari, N., Slason, I., Sodergren, E., Sonaike, T., Shim, C., Shooshtari, N., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalmson, A., Warren, R., Wall, R., Wang, S., Wart-Moore, S., Wart-Moore, S Unpublished 2 (bases 1 Direct Submission 1 to 154090)

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL Worley, K.C. Direct Submission

Direct Submission
Direct Submission
Submitted (25-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Aug 25, 2000 this sequence version replaced gi:9664948.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email of Molecular and Human Baylor Plaza, Houston, 3 (bases 1 to 154090) Submitted (11-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Worley, K.C.

REFERENCE

JOURNAL TITLE AUTHORS

COMMENT

gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the listing.

## ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts

Repeats are identified using RepeatMasker (A. Smit and P. Green

unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < le-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones an reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality a region does not meet this standard, it will be indicated in th annotation as Low Coverage. the and 2

Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases.

## QUALSTAT-REPORT------

Position 9347 91405 122290 137090 141632 cctagaaaaa(n)gacntttct gaaaaangac(n)tttctttt actgcaacct(n)tgcctcccag tttacatata(n)cagtacagta caacacaagn(n)taggtttggn ntaggtttgg(n)ttactcttcc agcaatgcag(n)ggctacagaa
ctttactatt(n)tgtttattct aacacagacc(n)tttttttt tcattgaccc(n)ctggtcattc ttactattnt(g)tttattctaa
acaacacaag(n)ntaggtttgg ctgtcaccag(n)aaaagatcca atttgcccct(n)taggaaaaga acagagaaag(n)caaaacactc tgaagccact(n)gaaaagtaat aaaaaaagaa (n)gtaagagaaa cacagcttaa(n)caaggtaaga tanttttttc(n)atctttaggg
accttagatg(n)ctcctcccag tttactattn(t)gtttattcta tttctttta(n)tttttcnat --- Consensus changing edits -----Original+Context tttactattt(g) itttattcta ttactatttg(t) ittattctaa acaacacaag(a) itaggittgg caacacaaga(t) itaggittggi ttaggittgg(t) itactcitcc tcattgacac(a) ctggicattc actgcaacct(c) igcctcccag cctagaaaaaa(t)gacttttct gaaaaatgac(t)ttttctttt tttctttta(t)tttttctat ctttactatt(t)gttttattct agcaatgcag(t)ggctacagaa ctgtcaccag(t)aaaagatcca aacacagacc(t)tttttttt aaaaaaagaa(a)gtaagagaaa cacagcttaa(a)caaggtaaga accttagatg(a)ctcctcccag tattttttc(t)atctttaggg tttacatata(a)cagtacagta Edited+Context

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                                                     CCAGCTGCTGCAGTGGCTGGCTGAAAGGGGCCAGCATAGAGCTTGGGCCGTGGCTTCGGAG
                                                                                                                                                                 GAGGTCTTCATGGCAGCCCATCCCATCACAGGCCCGGGGGCCTAGGAGAAAATGGTTTTG
                                                                                                                                                                               haaraaraayccnttywsngarggnaarttyaarytngcngcngarathtgyathtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                36.2%; Score 497.8; DB 9; ilarity 47.7%; Pred. No. 9.6e-109; Conservative 216; Mismatches 282;
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/chromosome="12"
/clone="RP11-13C3"
54...288
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2630. .2761
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8666. .8695
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8113
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complement(6678. .7.
/rpt_family="L1ME3"
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6571.
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/rpt_family="MER46B"
complement(1624. .1682)
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8385. .8587
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5232. .5301
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4088. .4216
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Et 1 (bases 1 to 18660)

RS Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Buck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bourch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, S., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, Z., Chowdhry, I., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Edranhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaggy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gaoriell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, J., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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JOURNAL
REFERENCE
AUTHORS
TITLE
BASE COUNT
ORIGIN
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Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., KureShi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.
Li, J., Li, L., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, L., Rolfe, M., Riiz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, 1.,
Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S.,
Williams, G., Wallamson, A., Washington, C., Watlington, S.,
Wulliams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D.,
Direct Suhmission
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Submitted (19-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 1, 2001 this sequence version replaced di.13877175
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                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h
NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye: 82% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 186630 bases at least Q40
Consensus quality: 186659 bases at least Q30
Consensus quality: 186660 bases at least Q30
Estimated insert size: 187779; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; sum-of-contigs estimation Quality coverage: 10.7x in Q20 bases; sum-of-contigs estimation
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Center clone name: RP11-307L1
----- Summary Statistics
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Sequencing vector: M13;
Sequencing vector: M13;
Chemistry: Dye-priner Bodipy: 18% of reads
Chemistry: Dye-terminator Big Dye: 82% of 1
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/db_xref="taxon:9606"
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Best Local Similarity 47.7%;
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                                                                                                                                                                        AAGAGGGAGCCTGTACCCTGCAAAGCCACAGAAGCAGAGCTTCCCAAGACCATGGGAACC
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TTTTGGCCAATTTCTCCCCATTTAGAACAGCTGTATTTACTCAATGCCTGTATCGCCATTG
                                                         ACTTTGAGATTTGACTACCCTTCTGGGTTTCAGACTTGCATGGGGCATATAGCCCCTTTG
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                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 29, 2001 this sequence version replaced gi:12584354.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL: Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 RPI1-279N8 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Direct S
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/clone_lib="RPCI-11.1"
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47.5%; Pre
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                                                                                                                                                            CCACCTCTTGCATCAGCATGACCTGGATGTGAGACATGGAGTCAAAGGAGATCATTTTGG
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  Query Match
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                                                                                                                                                                                                                                                                   * by the finished sequence as soon as it is available and the accession number will be preserved.

* the accession number will be preserved.

* 19436: contig of 9436 bp in length 9437 9536: gap of unknown length 26537: contig of 17001 bp in length 26538 26537: contig of 17001 bp in length 26538 45958: contig of 19321 bp in length 46058: gap of unknown length 46959 46058: gap of unknown length 68558 68757: contig of 22599 bp in length 68575: gap of unknown length 72153: contig of 3395 bp in length 72153: gap of unknown length 72153: gap of unknown length 81070 81169: contig of 8817 bp in length 81070 121547: contig of 40378 bp in length 121547: contig of 40378 bp in length 121547: contig of 40378 bp in length 121547: contig of 40378 bp in length
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Consensus quality: 116295 bases at least Q40

Consensus quality: 121288 bases at least Q30

Consensus quality: 122086 bases at least Q30

Estimated insert size: 122700; pulse field gel estimation

Estimated insert size: 122770; sum-of-contigs estimation

Quality coverage: 6.04 in Q20 bases; pulse field gel estimation

Quality coverage: 6.05 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 8 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes
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Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Project Information
Center Project Name: 651088
Center clone name: CITB-H1_2061E19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US: On Jul 18, 2000 this sequence version replaced gi:7709316.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome
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DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates;
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                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                       /clone_lib="CalTech human
24223 c 23855 g 36528
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                                                                                                                  /clone="CTD-2061E19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 22, 2000 this sequence version replaced gi:7543856. All repeats were identified using Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collin Collymore, A., Cooke, P., DeArellano, K., Dwar, K., Diaz, J.S. Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Gardyna, G., Gardyna, 
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Anderson, S., Baldwin, J.,
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Birren, B., Linton, L.,
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189768 bp
Homo sapiens chromosome 2 clone
SEQUENCE, 36 unordered pieces.
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consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                              NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815; 100% of reads Chemiatry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 180047 bases at least Q30 Consensus quality: 180404 bases at least Q30 Consensus quality; 184014 bases at least Q30
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                                                                                                                                                                                                                                                                   Quality coverage: 3.8 in Q20 bases; Quality coverage: 3.9 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L9594 Center clone name: 792_C_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center
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                                                                                                                                                                                                                                                                                                                                                                               Insert size: 190000; agarose-fp Insert size: 186268; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site: http://www-seq.wi.mit.edu
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Boukhgalter,B., Brown,A., Burkett,G.,
Boukhgalter,B., Collins,S.,
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J., Barna,N., Bastien,V., Beda,F.,
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as soon as in
be preserved
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                                  103319 112553; contig of 112554 112653; gap of 112654 112339; contig of 123240 123339; gap of 123340 137921; contig of 123340 133921; contig of 12
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Ja: gap of 1.
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04 27703: gap of 100 bp
11 30020: contig of 2317 bp in 1er
11 30120: gap of 100 bn
1 33472: con+17
                                                                                                 10 103318: contig of 6 19 103318: gap of 9 112553: contig of 4 11766
                                                                                                                                                                                                                   79286: contig of 6496 b
37 79386: gap of 100 bp
37 7938: gap of 4065 b
37 83451: contig of 4065 b
52 83551: gap of 100 bp
52 83570: contig of 8619 b
                                                                                                                                                                                                                                                                                                                                                                                                          3 51192: gap of 10
3 55262: contig of 4
3 55362: gap of 10
3 60982: contig of 5
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8145: contig of 1133
8245: gap of
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*1169: gap of 45266: ~~
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-: gap of
18527:
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790: gap of 100 bp
79286: contig of 6496
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41069: ~~
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67628: contig of
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22484: contig of 1823 bp in
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55363. .60982
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2385. .3898
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/db_xref="taxon:9606"
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86175 GAAAGGGGCCAACATAGAGCTCGGGCTGTGGCTTCAGAAGGTGCAAGCCCCAAGCCTTGG
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GGAACAGCTGTATTTACCCCATGCCTGTACCCCGATTGTA 85536
                        ggnacngcngtnttyacncartgyytntayytncaytgya 1375
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3 ACO17063 198545 bp DNA linear HTG 02-NOV-2001 ION Homo sapiens chromosome 4 clone RP11-354H17, WORKING DRAFT SEQUENCE, 4 unordered pieces.

ON ACO17063 ACO17063.7 GI:16596637 S HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.

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JOURNAL
REFERENCE
BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Nov 2, 2001 this sequence version replaced di:15741601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: H_NH0354H17
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Center code: WUGSC
Web site:http://genome.wustl.edu/9
Contact: submissions@watson.wustl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 10.58 in Q20 bases; agarose-fp Quality coverage: 10.55 in Q20 bases; sum-of-contigs
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Sequencing vector: plasmid; 65%
Sequencing vector: plasmid; 65%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number be preserved.
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4952: contig of 2136 bp in length
5052: gap of unknown length
198545: contig of 193493 bp in lengt
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2716: contig of 1442 bp in length
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.3; Mismatches 314;
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                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-primer ET; 81% of reads
Chemistry: Dye-terminator Big Dye; 19% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 144558 bases at least Q40
Consensus quality: 149743 bases at least Q30
Consensus quality: 152625 bases at least Q30
Consensus quality: 152625 bases at least Q30
Insert size: 176000; agarose-fp
Insert size: 188975; sum-of-contigs
Quality coverage: 3.48 in Q20 bases; agarose-fp
Quality coverage: 3.75 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission Submitted (07-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA On Jul 7, 2000 this sequence version replaced gi:7801489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161575 bp DNA linear HTG 07 HOMO sapiens chromosome 17 clone RP11-333E1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
AC025233
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1 (bases 1 to 161575)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; 10%
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----- Project Information
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HTG; HTGS_PHASE1; HTGS
                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McKernan, K., McFernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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Mammalia; Eutheria; Primates;
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AC087500.4 GI:18104839
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                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 17, clone RP11-333E1
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Direct Submission
Submitted (05-JAN-2001) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 10, 2002 this sequence version replaced gi:13560412.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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3135 3234: gap of 100 bp
27784 27883: gap of 100 bp
27884 50218: contig of 24349 bp in length
50219 50318: gap of 100 bp
50319 54526: contig of 4208 bp in length
54527 54626: gap of 100 bp
60201 60300: gap of 100 bp
60301 70374: contig of 10074 bp in length
60301 70374: contig of 10074 bp in length
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Contact: sequence_submissions@genome
------Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGAGCTGTGAGAAGAGGGCCAATGACCTCCAGACCCCAGAATGGTAGATCCACCTACAG 136850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nmgngcngtnmgnmgnwsnccnccnwsnwsnmgnytncaraarggnmgnwsnacngayws 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nmgnathgargtntgggarccnccnathmgnttycaraarathtayggnaayccntggat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gccnmgncaraarttygcngtnggngtnggnwsnwsntggmgnacnwsngcnmgngtngt
                                                                                                                                                                                                                            tyggncarttyttyccnttyggnacngcngtnttyacncar 1356
                                                                                                                                                                                                                                                                                                                                                                                            CCTCTTGCATCAGCATGACCTGGATGTGAGACCTGGAGTCAAAGGAGATCATTTTGGAGG
                                                                                                                                                                                                TTGGCCAATTTCTCCCATTTGGAACAGCTGTATTTACCCAG
Homo sapiens chromosome 17 clone RP11-420A6 SEQUENCE, 31 unordered pieces.
                                                                                                                                                                                                        137131
                                                       linear
6 map 17,
                                                         WORKING
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferrestra, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-terminator Big Dye; 96% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 161512 bases at least Q40
Consensus quality: 167866 bases at least Q30
Consensus quality: 170864 bases at least Q30
Consensus quality: 170864 bases at least Q20
Insert size: 170800; squaros-fp
Insert size: 172639; sum-of-contigs
Ouality coverage: 4.9 in Q20 bases
* NOTE: This is a 'working draft' sequence. It currently
consists of 31 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Direct Submission
Direct Submission
Submitted (17-NOY-1999) Whitehead Institute/MIT Center for Submitted (17-NOY-1999) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 9, 2000 this sequence version replaced g1:6958075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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          13948 14047: gap of 100 bp 114048 14259: contig of 212 bp in length 14260 14359: gap of 100 bp 114360 15039: contig of 680 bp in length 15040 15139: gap of 100 bp 15932: contig of 693 bp in length 15833 15932: gap of 100 bp 15933 16689: contig of 757 bp in length 1690 16789: gap of 100 bp 16993: contig of 1303 bp in length 16993 18192: gap of 100 bp 18993: contig of 1801 bp in length 18093 19993: contig of 1801 bp in length
                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and
                                                                                                                                                                                                                                                                                                                           be preserved
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Chemistry: Dye-ptimer Big Dye; 96% of reads
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center
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22305:

gap of

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81789 81888; gap of 100 bp 100 bp 11888 86479; contig of 4491 bp in length 86380 86479; gap of 100 bp 100 b
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                                                                                                                                                                                                                                                                                                             /note="assembly_fragment" 15140. .15832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment
clone_end:SP6
                                                                                                                                                        /note="assembly_fragment"
16790. .18092
       /note="assembly_fragment'
20094. .22205
                                                                              /note="assembly_fragment"
18193. 19993
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15933. .16689
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/clone_1ib="RPCI-11 Human
l. .13947
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/db_xref="taxon:9606"
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100 bp
113399; contig of 11379 bp
113399; gap of 100'
139546; conti
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28851: contig of 2207 bp in
28951: gap of 100 bp
30454: contig of 1503 bp in
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24015: gap of 10
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22205: contig of 2112 bp in length
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77528. .81788
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tive 202; Mismatches 280;
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                            Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgesh: CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 28, 2000 this sequence version replaced gi:11990058.
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----- Project Informa
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                                                 /note="assembly_fragment:00129
fragment_chain:1"
65541. .88588
                                                                                                    /note="assembly_fragment:00961
fragment_chain:1"
55726    .65440
fragment_chain:1"
88689. .94602
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fragment_chain:1"
                                                                                                                                                                                                                     vector_side:left"
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                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                      /note="assembly_fragment:02130
                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-11.2"
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181842: contig of 8639
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Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 4% of reads
Sequencing vector: plasmid; L08752; 95% of reads
Chemistry: Dye-terminator ET-amersham; 3% of reads
Chemistry: Dye-terminator ET-amersham; 3% of reads
Consensus quality: 17456 bases at least Q40
Consensus quality: 17456 bases at least Q30
Consensus quality: 177550 bases at least Q30
Consensus quality: 179392 bases at least Q30
Insert size: 180742; sum-of-contigs
Insert size: 162786; 7.7% error; agarose-fp
Ouality coverage: 4.40x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coverage: 4.89x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                       88589 88688: gap of 5914 bp in length 88689 94602: contig of 5914 bp in length 94603 94702: gap of 100 bp 94703 105410: contig of 10708 bp in length 105411 105510: gap of 100 bp 105511 107644: contig of 2134 bp in length 107645 107744: gap of 100 bp 107745 12686: contig of 18842 bp in length 107767 12668: contig of 18842 bp in length 107767 12668: contig of 18842 bp in length
                                                           126587 126686: gap of 100 bp
126687 155610: contig of 28924 bp in length
155611 155710: gap of 100 bp
155711 173103: contig of 17393 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8896: contig of 8896 bp in length
8897 8996: gap of 100 bp
8897 892635: contig of 13639 bp in length
22636 22735: gap of 100 bp
22736 55625: contig of 32890 bp in length
55626 55725: gap of 100 bp
55726 65440: contig of 9715 bp in length
65441 65540: gap of 100 bp
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bp in length
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snwsnmgngcngtnmgnmgnwsnccnccnwsnwsnmgnytncaraarggnmgnwsnacng
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fragment_chain:1"
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155711 .173103
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107745. .126586
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39941 c 37882 g 49105 t 1
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47.5%; Pred. No. 1.7e-106;
ative 212; Mismatches 290;
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source
                                                                                                                                     Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LO875; 100% of reads
Chemistry: Dye-terminator ET-amersham; 13% of reads Chemistry:
Dye-terminator Big Dye; 86% of reads
Consensus quality: 76604 bases at least 040
Consensus quality: 77098 bases at least 020
Consensus quality: 77320 bases at least 020
Insert size: 85298; 1.5% error; agarose-fp
Quality coverage: 4.54x in Q20 bases; sum-of-contigs Quality
coverage: 4.30x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes anger.ac.uk
On Aug 21, 2000 this sequence version replaced gi:9213111.
                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: bA435A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Sanger Centre
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                                     NOTE: This is a 'working draft' sequence This sequence will be replaced by the finished sequence as soon as it is the accession number will be preserved.
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                 Location/Qualifiers
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/map="g21.33-22.3"
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124531 bp DNA 11near PRI 07-FEB-2000 Human DNA sequence from clone 633H17 on chromosome 1p31.2-32.2. Contains a pseudogene similar to part of MTCO1 (Cytochrome C oxidase 1), MTCO2 (cytochrome c oxidase II), MTATP8 (ATP synthase 8) and GOT2 glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) pseudogenes, ESTs and GSSs, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was generated from part of bacterial clone contigs human chromosome 1, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl 633H17 is from the library RPCI-4 constructed at the Roswell Parl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence is ambiguous, there is an annotation using the 'unsure sequence sequence is an 
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Mammalia; Eutheria; Pr
1 (bases 1 to 124531)
                                                                                                                                                                                                                                       Em:, EMBL; Sw:, SWISSPROT; Tr:, TREME on the WORMPEP database can be found
                                                                                                                                                                                                                                                                                                                                   following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer Institute by the group of Pieter de Jong. For furthe details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requests: clonerequest@sanger.ac.uk
On Jul 29, 1999 this sequence versi
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/db_xref="taxon:9606"
                                                                                                                                       Location/Qualifiers
                                                     /organism="Homo
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                                                                                                                                                                                                                                                                                       SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP;
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/clone\_lib="RPCI-4"

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/note="AluSx repeat: matches 59.
complement(235. .546)
/note="match: GSS: Em:AQ055811"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ309712"
complement(16459. 16861)
/note="match: GSS: Em:AQ197233"
16531. 16576
/note="23 copies 2 mer tt 74% conserved"
18053. .18154
                                                                                                                                                                                                                                                                                                                          /note="MER81 repeat: matches 1. .110 of consensus" 20508. .20690
                                                                                                                                                              /note="L2 repeat: matches 2660. .2693 of 20828. .20863 . .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / .20863 / 
                                                                                                                                                                                                                                                                                              'note="LTR16C repeat: matches 190. .376 of
                                                                                                                                                                                                                                                                                                                                                                               /note="LTR16C repeat: matches 90. .152 of consensus"
20403. .20505
                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="MIR repeat: matches 28. .169 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 10. 9866. .20007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8377. .18492
/note="MER39b repeat: matches 476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16410. .16933
/note="match: GSS: Em:AQ357205"
16410. .17037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15157. .15818

'Moote="MER39b repeat: matches 14.

6403. .16945

note="match: GSS: Em:AQ454645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L2 repeat: matches 2585.
L4656. .14764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="L2 repeat: matches 2397.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MIR repeat: matches 114.
.3602. .13725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="MIR repeat: matches 74. .262
                                                                             'note="MER5A repeat: matches 56. .188 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MIR repeat: matches 7. .107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="MIR repeat: matches 124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L2 repeat: matches 2349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8525. .18954
note="match: GSS: Em:AQ210513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"MIR repeat: matches 130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L1PA2 repeat: matches 1. .6146 of consensus"
0000. .10124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1MA4 repeat: matches 5282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MIR repeat: matches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90. .11014
te="L2 repeat:
36. .11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :e="MIR repeat: matches 34.
23. .10689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e="match: GSS: Em:B30406" 6. .15150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="MIR repeat: matches 36. .102 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .14486
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                           repeat: matches 214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches 2389.
                                                                                                                                     matches
                                                                                                                                     40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .114 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .217 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2473 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2710 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2666 of
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                                                                                                                                     . 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .579 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of consensus"
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                           .285 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .574 of consensus*
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  35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .27868
                                                                                                                                                                                                                                                                                                                                                                                  .34334
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Score 488.2;
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/note="L2 repeat: matches 2578...2 2283...2259
/note="FRAM repeat: matches -2...1 22280...22393
/note="L2 repeat: matches 2541...2 2394...22748
/note="MLT1B repeat: matches 1...3 22749...22846
/note="L2 repeat: matches 2645...2 23644...27464
                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(31888. 3.2090)
/note="match: GSS: Em:B58153; match: match: GSS: Em:AQ759038"
32922. 33453
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23433. .23730
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33175. .33412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MSTD repeat: matches 1. .85 of consensus"
25557. .25651
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                                                                                  note="L1MC2 repeat: matches 5573.
                                                                                                                           note="MIR repeat: matches 20.
                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 2473.
3454. .33885
note="MLT1C repeat: matches 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="HERVL repeat: matches 1792. .2933 of consensus"
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10488. .30578
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8898. .27373
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note="L2 repeat: matches 2329.
3011. .23310
                                                                                                                                                                                                                note="MIR repeat: matches 129.
                                                                                                                                                                                                                                                      3947. .34302
note="THE1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                     note="MIR repeat: matches 162.
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0797. .31887
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note="L1PA13 repeat: matches 6011. .6152 of consensus"
9900. .30121
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matches
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  2638.
                                          2675.
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  .2707
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                                        GTTTTGGCCAATTTCTCCCATTTGGGAGGGCTATATTTACCCAATACTTGTACCCCCATT
                                                      gyttyggncarttyttyccnttyggnacngcngtnttyacncartgyytntayytncayt 1372
                                                                                                          CCTACCTCTTGCATCAGCATGACCTGGATGTGAGACCTGGTGTCAAAGGAGATCATTTTG
                                                                                                                                                                 CCAGGAGGGAGGCTGTACCCTGCAAAGCCACAGGGGTGGAACTGCCCAAGACTATGGGAA
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269722.1
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U212C1 is from the human chromosome X-specific cosmid library.
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Mammalia; Eutheria; P
1 (bases 1 to 40714)
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16026. .16155
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8954. .9088
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12171. .13985
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/clone="LL0XNC01-212C1"
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/db_xref="taxon:9606"
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                                                     /note="THE1B element
16624. .16722
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16204. .16495
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16073. .16149
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/note="L1_element
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/note="MSTA element fragment"
16651. .16712
                         /note="MSTC element fragment"
16626. .16737
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334 ytncaycaytgyaargtnaayathtggytnatgmgnaarcarathytngcnaayaargar 393
                                                    Conservative 225;
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40640. .40693
/note="27 copies of 2 mer 94 % conserved"
7879 c 8141 g 13150 t
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/note="THR element fragment"
24643. .25270
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28319. .28608
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26797. "26898
/note="MSTC element fragment"
27949. 28241
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25528. .25627
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25277. .25463
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23725. .24279
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/note="MLT1A element
23342. .23501
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19720. .19797
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32232. .32735
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23550. .23697
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ACCESSION VERSION KEYWORDS

AP004219.2

GI:18146615

RESULT 15 AP004219/c LOCUS DEFINITION

AP004219 1597
Homo sapiens genomic DNA,
complete sequence.
AP004219

159712 bp Dr NA, chromosome

DNA me 8q23,

linear clone:

PRI 26-DEC-2001 KB1222D11,

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/rpt_fa /evider 11063. /rpt_fa /evider 11301. /rpt_fa /ev1der /rpt_fa /rpt_fa	_region _region	repeat_region 68607158 /rpt_family="AluJo" /rpt_family="AluJo" /evidence=not_experimental repeat_region /rpt_family="AT_rich" /evidence=not_experimental repeat_region 91889226 /rpt_family="AT_rich" /evidence=not_experimental repeat_region complement(92279522)	repeat_region 64106589  /rpt_family="FAM" /evidence=not_experimental repeat_region 66196648 /rpt_family="AT_rich" /rpt_family="AT_rich" /evidence=not_experimental repeat_region complement(66496776) /rpt_family="ALUJO/FARM" /evidence=not_experimental		/chromosome="8" /chromosome="8" /chome="RB123" /clone="RB122Dl1" /cell_line="FLEB 14 - 14" /cell_tipe="pre-pro-B cell" /cell_type="pre-keio BAC library" repeat_region 1. 4242 /rpt_family="L1PA2" /evidence-not_experimental repeat_region 4668. 4733	OI Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizu@dmb.med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)  COMMENT On Jan 14, 2002 this sequence version replaced gi:15824050.  FEATURES Location/Qualifiers 1. 159712  Source /organism-"Homo sapiens"  /db xref."taxon:9606"	e-pro-B cell cell_line:FLEB 14 - 14 DNA, BAC library clone:KBl222Dl1. zoa; Chordata; Craniata; Vertebrata; Euteleostoria; Primates; Catarrhini; Hominidae; Homo. 159712) Asakawa, S. on on 159712) Nobuyoshi Shimizu, Kelo University, Son
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Query Match
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RHD gene deletion in Rh negative haplotypes. The Rhesus genes

locus comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the

Rhesus box(es), preferably the hybrid Rhesus box, the upstream Rhesus box

and/or the downstream Rhesus box. The RHD and RHCE genes are located at

chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the

RHD deletion in the common RHD negative haplotypes. The sequence has

been used to design primers which are useful for: (1) the specific

detection of the common RHD positive haplotypes in D-negative

individuals; (2) blood group typing; (3) determining whether a patient

can be transfused with RhD negative blood and whether blood is suitable

for transfusion to patients who should not be exposed to antigen C; (4)

assessing the risk of a RhD negative mother of conceiving or carrying an

RhD positive foctus. Anti-D antibodies are useful for treating pregnant

women who are Rhesus D negative, where the foetus is not homozygous for

the RHD gene to treat or prevent haemolytic disease of the newborn.
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31-MAY-2000;
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Pred. No. 2.
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                           The sequence represents the coding sequence of Rhesus gene locus: downstream Rhesus box of D positives. The Rhesus genes locus comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the Rhesus box (es), preferably the hybrid Rhesus box, the upstream Rhesus box and/or the downstream Rhesus box. The RHD and RHCE genes are located at chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the RHD deletion in the common RHD negative haplotypes. The sequence has been used to design primers which are useful for: (1) the specific detection of the common RHD positive haplotypes in D-negative Individuals; (2) blood group typing; (3) determining whether a patient can be transfused with RhD negative blood and whether blood is suitable for transfusion to patients who should not be exposed to antigen C; (4) assessing the risk of a RhD negative mother of conceiving or carrying an assessing the risk of a RhD negative mother of conceiving or carrying an
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                                                                                                                                                                                                                                                                   893
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                                                                                                                     TIGITIGGCCAGGCCCGGGGTCCTCATGCTGTGCAGCCTAGGGACTTGGTGCCCTGCAT
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GAGCTTTAAGATTTGACTGCCCCACTGGATTTTGGACTCTCATGGGCCTGTAGCCTCTTT
          thtayytnytncaytgycaygayytngaygtnmgncayggngtnaarmgngaycayttyg
                                                                                          cnggnatggarwsngtnccntayaaracngtngtngcngarytnacnaaracngtnggna
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                                                                              CTGAGAGGGAGGCTGTACCCTGCAAAGGTACAGGGGCAGAGCTGCCCAAGACCATGGGAA
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Pred. No. 2.7e-103;
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rgargarathwsnaarcarcarwsnathcargargtnacntgggtnytnytnaargcntt 449

Query Match Best Local S Matches 485

Similarity

32.8%;

Score 452; DB 22; Pred. No. 2.7e-103; Pred. No. 282;

Length 9241;

Inde1s

45;

Gaps

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Conservative

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              Sequence
                                                                                                                  Disclosure;
                                                                                                                              and
                                                                                                                                    New
RHD
                                                                                                                                                     WPI;
                                                                                                                                                                                        02-NOV-1999;
31-MAY-2000;
                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                         Rhesus box; RHD positive; sequence length polymorphism; SSP; IRHCE; Rh negative; blood group typing; blood transfusion; antihaemolytic disease of the newborn; chromosome 1 p34.1-p36; ds
                                                                                                                                                                                                                                                                                                                      AAS03688 standard; DNA; 9241
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                                                                                                                                                                                                                                                                                  Rhesus gene
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                                                                                                                                  nucleic acid molecular positive haplotypes in
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          RHD gene
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9241 BP;
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                                                                                                                                                                                        99EP-0121686.
2000EP-0111696.
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                                                                                                                                                                                                                                                                                             (first entry)
          to treat or prevent
2454 A; 2320 C;
                                                                                                                                                                                                                                                                                  Rhesus
                                                                                                                                  structure,
D-negative
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                                                                                                                                                                             BADEN WUERTTEMBERG
          haemolytic disease of the newborn.
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2014 G;
                                                                                                                                   individuals, comprises RHD, SMP1
                                                                                                                                                                                                                                                                                  RHD negatives
2453
Τ;
0 other;
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SEQ ID NO:24

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                                                                           GTTTTGACCAATTTATCCCATTTGGAATGGCTGTATTTACCCAATGCCTGTACCCCCATT
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amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 24 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, anglogenic disorders, kidney disorders.
                                                                                                                                                                                                         The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                  AAD05121-AAD05203 represent cDNAs corresponding to 24 human secreted protein genes, and AAE01232-AAE01311 represent the proteins they encode. AAE01312-AAE01340 represent human secreted protein variants or fragments
                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1999;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder;
         gastrointestinal disorders, pregnancy-related disorders, disorders, and infections. The proteins can also be used
                                                                                                                                                                                                                                                                                                                                                used
                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         foetal abnormality; developmental abnormality; haematopoietic disorder;
immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                               isolated nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partner identification; ss.
                                                                                                                                                                                                                                                                                                                                             preventing,
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2000US-0215130.
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153..215
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153..356
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2000US-0225268
2000US-0225277
2000US-0225447
2000US-0225775
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2000US-0186628.
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2000US-0205515.
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2000US-0228924.
2000US-0229387.
2000US-0229344.
2000US-0229344.
2000US-0229513.
2000US-0230437.
2000US-0230438.
2000US-0231242.
2000US-0231243.
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10-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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                                                                                SPINK5; lympho-epithelial Kazal-type related inhibitor; LEKTI; protease inhibitor; atopic disease; Netherton's syndrome; asthr, hayfever; antiasthmatic; antiallergic; antiinflammatory; blogical; PCR primer; sequencing primer; gene therapy.
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crayments of a SPINK5 clone, sequencing primers and PCR primers for C SPINK5. SPINK5 encodes lympho-epithelial Kazal-type related inhibitor (LEKTI), a serine protease inhibitor. Susceptibility or predisposition to an atopic disease in a human subject can be detected by screening the genome for one or more polymorphic variants of SPINK5 gene and/or expression of a variant LEKTI protein in a tissue. Carrier status of a subject or development of Netherton's syndrome is diagnosed by screening for the presence of loss-of-function mutations in the SPINK5 gene. An expression vector comprising a nucleic acid encoding a serine protease inhibitor or its functional fragment can be used in screening for compounds with potential pharmacological activity by determining the serine protease activity of a protein previously identified as a ligand of the LEKTI protein. The atopic diseases include Netherton's Syndrome, casthma, eczema and hayfever.
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in SPINK5, a (
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Determining susceptibility to atopic disease or carrier status of Netherton's syndrome in humans by identifying variants of or mutain SPINK5, a gene encoding lympho-epithelial Kazal-type related
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Sequences AAS44359-AAS44514 represent the SPINK5 gene, contigs and carriers of a SPINK5 clone, sequencing primers and PCR primers for SPINK5. SPINK5 encodes lympho-epithelial Kazal-type related inhibitor (LEXTI), a serine protease inhibitor. Susceptibility or predisposition to can atopic disease in a human subject can be detected by screening the genome for one or more polymorphic variants of SPINK5 gene and/or expression of a variant LEXTI protein in a tissue. Carrier status of a subject or development of Netherton's syndrome is diagnosed by screening for the presence of loss-of-function mutations in the SPINK5 gene. An expression vector comprising a nucleic acid encoding a serine protease inhibitor or its functional fragment can be used in screening for compounds with potential pharmacological activity by determining the serine proteats activity of a protein previously identified as a ligand of the LEXTI protein. The atopic diseases include Netherton's Syndrome, as the account and hardener.
                                                    eczema
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                                                    and
                                                    hayfever.
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Sequence.

31529

BP; 9686 A; 5798 C;

5934 G;

10111 T;

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DB 22;

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31529

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RESULT 10
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     reproductive system related antigen; reproductive system disorder; gene therapy; ds.
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t Local Similarity
ches 475; Conserva
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                            Human; primer;
                                                                  26-JUN-2001
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                                              cDNA sequence
                                                                                                      standard;
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                                                                  (first
                            detection;
                                               SEQ ID NO: 10539.
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                            diagnosis; antisense therapy;
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                           therapy;
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09-JUN-2000;
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Ishii
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full-length
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27-AUG-1999;
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rmgnwsnwsncarcarwsnathaarwsnytngcntggmgnccnmgnmgnaartggttytg
                                                                     agacaagaaaaacccattttctggggagagattcaagccagctgcggaaatttgtgtaag
                                                                                                                                                                                                                              tagttttataagggaagcagagcataaaagtttggaaaatttgcagcattactatgcgat
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                                             tagcaaggagcctaatgttagtccccaagaccatggggaagatgtctccagaccatgtca
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2000JP-0183767.
2000JP-0241899.
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T, Wakama
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  C(II). (II) is useful for generating antibodies against it detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical cimaging of sites expressing (II). (I) and (II) are useful for treating continuity of the polypeptide and polynucleotide sequences have applications in cidagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human cidagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 458; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                new isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to associate biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
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immune system disorder; AIDS; autoimmune disease; rheumatoid ar inflammation; allergy; neurological disorder; Alzheimer's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy related disorder; gastrointestinal disorder; pregnancy related disorder;
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endocrine disorder; infection; wound healing; vulnerary;
cell culture; chemotaxis; food additive; gene therapy;
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Best Local
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30-JUN-2000; 2000US-0215130.
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Local Similarity 45.8%; P
mes 458; Conservative 205;
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aggtcttcatggcagcccctcccatcacagaccctgaagactaggaggaaaaaatggttt
                                                    mgnwsnwsncarcarwsnathaarwsnytngcntggmgnccnmgnmgnaar---tggtty
                                                                                                                                                  cattttaaaagggaaac--agcataaaaatttggaaaatttgcagccagttgatgcagca
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Pred. No. 4.8e-
5; Mismatches
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298;
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31-MAR-2000;
23-AUG-2000;
                                                                                                                       Human; chromosome mapping;
food supplement; medical i
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AAS87262 standard; cDNA; 1580
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                                30-MAR-2001;
                                                                                                Homo sapiens.
                                                                                                                                                     DNA encoding novel human diagnostic protein #23066.
                                                                                                                                                                           13-FEB-2002
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                                                                                                                     supplement;
  2000US-0540217
2000US-0649167
                                 2001WO-US08631
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                                                                                                                       imaging;
                                                                                                                       gene mapping; gene
maging; diagnostic;
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for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and mino acid sequences. AAS64197-AAS94564 represent novel human according sequences of the invention.

CC specification, but was obtained in electronic format directly from WIPO appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Simi
Matches 466;
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724
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Local Similarity 42.4%; Pred. No. 7.6e-91;
les 466; Conservative 215; Mismatches 383; Indels 34;
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                                                                                                                                                                                                                                                                                                                                                               AATCTGCAGCATGACAGTGCAATAGAAAAAGAAAAACCCATTTTCTGGGGAGAAATTCAAG
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ccnmgngayytngtnccntgygtnccngtnaaywsng----
                                                                         AGGCCTAGGAGGAAAATATGGTTTTGTGGGCCTGGGCCCAGGACCTTGCTGCTTTGTGCAG
                                                                                                            mgnccnmgnmgnaa---rtggttytgyggnacnggnccnggnwsnytntgytgygtncar
                                                                                                                                                                                                                        AAAAATGTTTTCAGGGCACGTCAGAGACCCTTATGCCAGCCCCTCCCCATCGCAGGCCCAG
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: Dehlinger & Associates

ADDRESSEE: Theidage Avenue, Suite
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         US-08-991-789A-29
Sequence 29, Application US/0899178; Patent No. 6225054; GENERAL INFORMATION: Frudakis, Tony N.; APPLICANT: Frudakis, Tony N.
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14378 CCTGTATCCCCATTGTAT 14361
                                                                                                    14438
                                                                                                                                                            14498 GGAGATCATTCTGGAGCTTTAAGATACACCTGCCCCACTGAATTTCGGACTTGCACGGGG
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08
FILING DATE: 26-JAN-1996
ATTORNEY AGENT INFORMATION:
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nes 221; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1ND1VIDUAL 1SOLATE:
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                                                       yytntayytncaytgyat 1376
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(415) 324-0960
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hes 172;
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Application US/08991789A

Smith, oc.

John M.

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 29
US-08-991-789A-29
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Best Local :
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1240 mgngaycayttyggngcnytnmgntt----ygaytgyccnacnggnttymgnacntayat 1295
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Seed IP Law Group
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                                                                                                   aracngtnggnathtayytnytncaytgycaygayytngayg-tnmgncayggngtnaar 1239
                                                                                                                                                                                                                                                              ACCCACCAAAAACTTATGCCATATTGCCTATAAAACCTACAGACACTCAATGCCAGCCCC 362
                                                                                                                                                                                                                                                                                                                                                                  AACACTGCCT AATGAAACTGTGAGAAGATGGCCACTGTCATCCAGACACCAGAATGATAG
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                                                     AGGCCATGGAAGCACAGCTCTTATATCAATGTGACCTGGATGTTGAGACATGGAATCCNA 482
                                                                                                                                                        ATGAAAAAAAAAACTGAGAAGAAGACTGTNCCCTACAATGCCACCGGAGCAGAACTGCCCC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
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US-09-062-451-29
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                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: Frudak
APPLICANT: Smith,
APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/29/062,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS ATTITLE OF INVENTION: TREATMENT AND NUMBER OF SEQUENCES: 297
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                                                                                                                                                                                                                   772 garggngcnwsnccnaarccntggcarytnccnwsnggngtngarccngtnggngcnaar 831
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                                                                                                                                                                                                                                                                   / Match 12.0%; Score 164.6; Local Similarity 40.7%; Pred. No. 1.66 res 250; Conservative 105; Mismatches
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ZIP: 98104-7092
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CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                3 GAGGGTACCAGCCCCAAGCCTTGACAACTTCCATAGGGTGTCAAGCCTGTGGGTGCACAG
ngcnmgngtngtncaraarggnaaygtnggntgggarccnccncaymgngtnccnwsngg
                                                       TAACACCTAGATATTCAGACAAAAGTTTACTACAGGGATGAAGCTTTCACGGAAAACCTC 182
                                                                          naayccntggatgccnmgncaraarttygcngtnggngtnggnwsnwsntggmgnacnws 944
                                                                                                                            AGTCAAAAATTGAGTTTTGGGATCCTCAGCCTAGATTTCAGAGGATATAAAGAAACACC 122
                                                                                                                                                  aarwsnmgnathgargtntgggarccnccnathmgnttycaraarathtaygg------ 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frudakis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tony N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210121.41902
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nes 243;
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GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 REI
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT FILING DATE: 1998-08-03
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER APPLICATION NUMBER: US 60/094,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
COMMENDE: ESCITED 65-05-05-06-04
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                                                                                                                  В
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NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A, 5
S-09-128-155-16
                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 324; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 16
LENGTH: 152331
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                  Score 140.6; DB 3;
Pred. No. 2.1e-27;
58; Mismatches 426;
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                                                                                                                                                                                                               Length 152331;
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US-08-687-080-59; Sequence 59, Application; Patent No. 5965427
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                                                                                                    APPLICANT: Gregory Dolganov TITLE OF INVENTION: Human Ri
                                                                        CORRESPONDENCE ADDRESS:
                                                                                          NUMBER OF SEQUENCES:
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INFORMATION FOR SEQ ID NO: 55
SEQUENCE CHARACTERISTICS:
LENGTH: 14855 base pairs
TYPE: nucleic acid
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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APPLICATION NUMBER: US 08
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
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nes 191; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 4600-0111.30
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                                       CTAGATTTCAGGGGATGTATGGAAACGTCTGGATGTCCAGGCAGAAGTCTGCAGGACTTG
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%; Pred. No. 4.9e-27
101; Mismatches 16
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US-08-232-463-14/c
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Best Local S
Matches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMTELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DORNER, F. APPLICANT: SCHEIFLINGER, F. G. APPLICANT: FALKNER, F. G. TITLE OF INVENTION: RECOMB NUMBER OF SEQUENCES: 52
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MEDIUM TYPE: Floppy disk
IMMEDIATE SOURCE:
CLONE: pTZgpt-
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LENGTH: 7218 base pairs
TYPE: nucleic acid
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PRIOR APPLICATION NUMBER: 1
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                               406 carcarwsnathcargargtnacntgggtnytnytnaargcnttywsnttyathmgngar 465
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Alexandria
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1800 Diagonal Road,
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(703)683-4109
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US-09-106-194-11
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            Query Match 4.3%; Score 59; DB 4; L6 Best Local Similarity 9.3%; Pred. No. 3.5e-06; Matches 101; Conservative 297; Mismatches 676;
                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Durnam, Diane
APPLICANT: Blumberg, Hal
TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: ZPPAR4
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Leith, Debra K
REGISTRATION NUMBER: 32,
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CITY: Seattle
STATE: WA
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                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                            LENGTH:
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1201 Eastlake Av
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Durnam, Diane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTNGARMGNCCNCCNGGNCARGTNWSNYTNGCNGCNCCNTTYYTNCCNGTNACNGARCAR
                                                                                                                                                                                                                                                                                                                                                                      TGYGARGGNTGYAARGGNTTYTTYMGNMGNWSNCARCARAAYAAYGCNWSNTAYWSNTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ayytngtnccntgygtnccngtnaaywsngcngtngcnwsngarggngcnwsnccnaarc
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cntaya
                                                                                               GARCARMGNCARCARWSNGGNGARGCNGARGCNYTNGCNMGNGTNTAYWSNWSNWSN 1020
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                                                                                                                                                                                      tnggntgggarccnccncaymgngtnccnwsnggngcnccnwsnwsnmgngcngtnmgnm 1030
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                                 ATHWSNAAYGGNYTNWSNAAYYTNAAYAAYGARACNWSNGGNACNTAYGCNAAYGGNCAY 1080
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                                                                                                                                                                                                                                    YTNCARAARTGYYTNGCNYTNGGNATGWSNMGNGAYGCNGTNAARTTYGGNMG···NATG
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RESULT 10
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Patent No. 5869330
GENERAL INFORMATION:
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Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1313 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Scherer, Philipp E. APPLICANT: Lodish, Harvey F.
                                                                                                                                                                                                                 158 gyccngayathgarmgnwsngcnttyacngtnaarytnwsnggnaarytnccnytnccnt 217
                                                                                                                                                                                                                                                                                            392 GTGCCTATGTATACCGCTCAGCATTCAGTGTGGGATTGGAGACTTACGTTACTATCCCCA 451
                                                                      572 ATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACA 610
                                                                                                        338 aycaytgyaargtnaayathtggytnatgmgnaarcara 376
                                                                                                                                              512 CTGGTAAATTCCACTGCAACATTCCTGGGCTGTACTACTTTGCCTACCACATCACAGTCT 57:
                                                                                                                                                                  278 tgggngtnttygcntgymgngtnccnggnaaytaytaywsnwsnttygaygtngarytnc 337
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A NOVEL SERUM PROTEIN PRODUCED
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NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 4517
TYPE: DNA
ORGANISM: Homo sapiens
US-09-140-804-9
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US-09-053-866-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.8%; Score 51.8; DB 4 Best Local Similarity 34.2%; Pred. No. 0.0008; Matches 75; Conservative 36; Mismatches 10
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APPLICANT: Xu, We
APPLICANT: Presne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sheppard, Paul O. APPLICANT: Humes, Jacqueline M.
                                CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                          ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,866
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Foster, Donald C.
TITLE OF INVENTION: PROTEASE-ACTIV
TITLE OF INVENTION: PAR4 (ZCHEMR2)
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
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APPLICANT:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                    COUNTRY: US
ZIP: 98102
                                                                                                                                                                         COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                             STATE: WA
                                                                                                                                                                                                                                                                                                            STREET: 1201 |
CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                         USA
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Yee, David P.
                                                                                                                                                                                         IBM Compatible
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Best Local :
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REGISTRATION NUMBER: 32,619
REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
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LENGTH: 1155 base pairs
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STRANDEDNESS: single
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Local Similarity 6.3%; Pred. No. 0.00046;
es 64; Conservative 256; Mismatches 703; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NACRAARAANGCNACNGCNSWNGCNARNACNACNGCNGTNARNCKNARNGCRTGNCCRTA
arcaygtnccngaraarwsnacngayacncartgycarccngtnaargcngcnggnatgg 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGTYTGNCKYTGNARNGTNARNGGNARNGCNARNGCNGCCATNARCCANGCNGCCAT
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                                                RTTCATNARNARCATNGTNSWNGGNARNCKNGGNGCYTGNGTNGCNARNACCCANARNGC
                                                                                            cngtnmgnmgnwsnccnccnwsnwsnmgnytncaraarggnmgnwsnacngaywsnytnc 108
                                                                                                                                               NARRTGRTANGCDATNCKNGGNGGNARNGCNARNGCNARNARRTCNGCNGTNGCNAR
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                                                                                                                                                                                                                                                                                      gncaraarttygcngtnggngtnggnwsnwsntggmgnacnwsngcnmgngtngtncara
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; NAME/KEY: misc_feature
; LOCATION: (1)...(2082)
; OTHER INFORMATION: n = A,T,C or
US-09-440-325A-2
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US-09-440-325A-2
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Best Local S
Matches 82
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LENGTH: 2082
TYPE: DNA
ORGANTTO:
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GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-11-15
NUMBER OF SEQ ID NOS: 3
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TITLE OF INVENTION: 20
FILE REFERENCE: 98-79
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616 acnttygarcaytaygtngarytnwsnaayaargcngcncarytnaayggngtnnnnaar
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                                      snytngcntggmgnccnmgnmgnaartggttytgyggnacnggnccnggnwsnytntgyt
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10.4%; Pred. No. 0.0026;
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GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Baindur, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/351,414
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
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                                                  Query Match
Best Local Similarity
Matches 140; Conserv
                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2088)
OTHER INFORMATION: n = A,T,C or
-09-351-414-3
                                                                                                                                                                                                           FEATURE: NAME/KEY: variation
                                                                                                                                                                                                                                                             LENGTH: 2088
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                   LOCATION: (1)...(2088)
OTHER INFORMATION: n is any
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                                                  3.5%; Score 48.8; DB 4; Length 2088; 11.8%; Pred. No. 0.0026; ative 286; Mismatches 749; Indels 8
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EARLIER APPLICATION UNMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 17
LENGTH: 289
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NAME/KEY: misc_feature

: LOCATION: (1)...(289)

: OTHER INFORMATION: n = A,T,

US-09-007-005-17
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             Sequence 17, Application US/09244796
PATENT NO. 6281344
GENERAL INFORMATION:
APPLICANT: SZOSTAK, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
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APPLICANT: SZOSTAK, Jack W.
APPLICANT: ROberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
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Best Local Similarity
Matches 27; Conserv
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CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
  CURRENT
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ORGANISM: Artificial Sequence
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NUMBER:
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US/09/244,796
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; OTHER INFORMATION: n = A,T,C US-09-244-796-17
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EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 17
LENGTH: 289
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Best Local Similarity
Matches 27; Conserv
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and is derived by analysis of the total score distribution.
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AQ239408	BM449699	AW857140	BG681769	BG679573	AG104336	AG001229	AU140358	AG096655	B94403	AL602279	AG075663	AG001408	AG057341	AG119684	AQ020199	AG070563	BI916691	AG045131	BE728616	AG125093	·AG115932	BM451317	BG761979	AG018926	BG281182	BM045873	AQ588873	
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## ALIGNMENTS

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JOURNAL COMMENT
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AUTHORS
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                                                           Query Match 34.8
Best Local Similarity 47.1
Matches 500; Conservative
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Unpublished (2000)
Unpublished (2000)
Contact: xingwu Lu,liangxian Cui,yonghai Li
Contact: xingwu Lu,liangxian Cui,yonghai Li
Department of Biochemistry
Institute of Basic Medical Science, Peking Union Medical College
NonaDan SanTiao 5, Beijing, P.R.C, 100005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
BE420422
BE420422.1
EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DDRT-PCR from B cell
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32-393 human
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full-length and coding sequence.
Cocation/Qualifiers
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/clome_lib="human bone marrow cDNA library"
/tissue_type="bone marrow"
531 c 641 g 738 t
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47.1%; Pred. No. 4.6e-98;
tive 222; Mismatches 299;
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TITLE
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IMAGE:3831313, 1
BC004496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 14 Row: d Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephan Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/note="Vector: pOTB7"
429 c 513 g
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/clone_lib="NIH_MGC_20"
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/db_xref="taxon:9606"
/clone="IMAGE:3831313"
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                                                                                                                                                                                                                                                                                                                                                                                   AGCCGCAGACATTCAACACCAGCCCGTGAAAGCAGCCAAAAAGGGGGGAATATATCCTGCAA
                                                                                                                                                                     sequence.
BE512633
                          Unpublished (2000)
Contact: xingwu Lu,llangxian Cui,yonghai Li
Department of Biochemistry
Institute of Basic Medical Science, Peking
Dongban Sanriao 5, Beijing, P.R.C, 100005
Tel: 86-010-65295951
Email: luxingwu@263.net
                                                                                    Lu,X., Cui,L. and Li,Y.
DDRT-PCR from B cell
                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1514)
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BE512633.1
                                                                                                                                                                                     BE512633
32-1514 human
                                                                                                                                            numan.
                 cDNA sequence.
                         luxingwu@263.net
          Location/Qualifiers
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B lymphocyte cI
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427; Conserv
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                  TTGTTTTACTCAATTTCTCCCATTTGGAACAGCTGTGTTTACACAATACCTGTACCCCCA
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/db_xref="taxon:9606"
/clone_lib="human B lymphocyte
/tissue_type-"bone marrow"
1 341 c 398 g 395 t
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Pred.⊘No. 1.1e-79;
2; Mismatches 256;
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yytngtnccntgygtnccngt
                                          GAGGAAAAAGAGGTTTCGTGGGCCCAGGCCCAGCATCCCCGTGCTTTGTGCAGCCTAGGGA 241
                                                      nmgnmgnaartggttytgyggnacnggnccnggnwsnytntgytgygtncarccnmgnga 731
                                                                                                 GTCTCCGGGCCATGTCAGAGACCTTCATGGCAGCCCCTCCCATCACAGGCTGGAGGCCAG
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BI488505
BI488505.1 GI:15327733
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603021014F1 NIH_MGC_114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 870)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11479 row: k column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                       222
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Location/Qualifiers
                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                  /note-*Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:5191803"
/clone_1ib="NIH_MGC_114"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 7.2e-66;
51; Mismatches 273;
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                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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BM472108
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                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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1 (bases 1 to 1050)
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                                                                  High quality sequence stop:
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/organism="Homo sapiens
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Primates;
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MAGE:5539381
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Matches 335; Conservative
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Cryan: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/notice="Cryan: skin;
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1 (bases 1 to 1036)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Ge
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re(mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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5', mRNA sequence.
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BM471183.1 GI:18520225
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Plate: LLAM12293 row: g column: 18
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/note="Organ: skin; Vector: pCMV-SPRT6; Site_1: Not1;
/note="Organ: skin; Vector: pCMV-SPRT6; Site_1: Oligo:
/note="Organ: skin; Vector: pCMV-SPRT6; Site_1: Oligo: Site_2: Sall; Cloned unidirectionally. Primer: Oligo: Average insert size 2 kb. Library constructed by Life
Technologies."

239 c 294 g 247 t 2 others
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/clone="IMAGE:5563049"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
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/db_xref="taxon:9606"
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Pred. No. 2.1e-62;
6; Mismatches 267;
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AGENCOURT_6411690 NIH_MGC_92
5', mRNA sequence.
EM457166
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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Plate: LLAM12346 row:
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High quality sequence stop: 713.
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone_lib="NHLMGC_92"
/clone_lib="NHLMGC_92"
/tissue_type="embryonal carcinoma, cell line"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCWV-SPORT6; Site_1: NotI;
/note="Organ: testis; Vector: pCWV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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AG086951.1 GI:16638753
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-085H08.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Totoki,Y., watanabe,H. and Sakaki,Y.

Direct Submission
Submitters 'Cr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H: and Sakaki,Y.
BAC end sequences of Library PTB
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Pan.
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R.Site 2 : SacI
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/clone_lib="PTB Chimpanzee Male
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/sex="male"
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/db_xref="taxon:9598"
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Query Match 22.3%; Score 306.6; DB 10; Best Local Similarity 44.1%; Pred. No. 5.1e-59; Matches 306; Conservative 122; Mismatches 266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Platte: LLAM11485 row: g column: 21
High quality sequence stop: 733.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5194028"
/clone_lib="NIH_MGC_1114"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                /note="Organ: brain; Vector:
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AG112666 AG112666 GS; GSC (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone: PTB-119801.R.
and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC en
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                 Submitted (02-AUG-2001) Asao Fujiyama,
                                                                                                                                                                                         Totoki,Y., Watanabe,H. and
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Totoki, Y., Watanabe,
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/sex="male"
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/clone_lib="PTB Chimpanzee Male
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                                                   GGTAGATCCACTGACAGCTTACACCATGTGCCTGAAAAAGCTGTAAACACTCAACACCAG
                                                                                                                            ACTGGGGCACCATCTAGTGGAGCTGTGAGAAG - AGGGCACTGACCTCCAGACCCCAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (O2-AUG-2001) Asao Fujiyama, The Institute of Physical Submitted (O2-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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AG064424.1 GI:16616226
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-053H24.R.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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2 (bases 1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/clone_lib="PTB Chimpanzee Male
165 c 191 g 156 t
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/clone="PTB-053H24.R"
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Pred. No. 1.3e-56;
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                                                                                                                                                                                                                                                                                                                                                                                               and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
17-22 Sushiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp/,
URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-050M20.F.
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                                                       Similarity 49.001; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAC end sequences of Library PTB
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                                                                                                                                              /Cell_type="lymphoblast"
/Clone_lib="PTB Chimpanzee Male
167 c 201 g 162 t
                                                                                                                                                                                                            /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-050M20.F"
                                                                                                                                                                                                                                                                         Location/Qualifiers
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Primates;
                                                         Score 287.4; DB 12;
Pred. No. 1.2e-54;
10; Mismatches 196;
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Catarrhini; Hominidae;
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                           Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC encloses are derived from the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                              AG116938 720 bp DNA linear GSS 03-NOV-200. Pan troglodytes DNA, clone: PTB-124K01.R, genomic survey sequence. AG116938 AG116938.1 GI:16737457 GSS; GSS (genome survey sequence). Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Malacclibrary clone:PTB-124K01.R.
                                                                                                                                      2 (bases 1 to 720)
Fujiyama, A., Hattori, M., Toyoda, A.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                     Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                           BAC end sequences of Library PTB
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                          clone tracking errors.
                                                                                                                                                                              Unpublished
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   Sequencing:
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                                                                                                                                                    Taylor, T.D.,
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AQ037711
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CIT-HSP-2337G10.TR CIT-HSP Homo
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TCTGTATTCCCATT 720
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                            yytntayytncayt 1372
                                                                                                                             GAGACCATGGGAACCTACCTCTTGCATCAGGGTGACCTGGATGTGAGACATGGATTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                            ACTGGGG-ATCACCTAGTGGAGCTGTGAGAAGACAGCCACTGTCTTCCAGACCCCCAGAAT 408
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/db_xref="taxon:9598"
/clone="PTB-124K01.R"
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186 c 187 g 165 t
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Pred. No. 2.3e-54;
.2; Mismatches 200;
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GI:3303543

sapiens genomic clone 2337G10, DNA

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                 ncaytgycaygayytngaygtnmgncayggngtnaarmgngaycayttyggngcnytnmg
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TTATGCAACTGGAAAAGCCACAGACACTCAACACCAGCCCATGAAAACAGCCAGGAGGGG 385
                                                                                                                                                                                                                                                                                                               rggnaaygtnggntgggarccnccncaymgngtnccnwsnggngcnccnwsnwsnmgngc
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                                                                                          GGGAAATGTGGGGGTTGGAGCCGTCACAGAGAGTCTCTACTGGGGCACTGCCTAGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                   GCAAAAGTTTGCTGCAGGGGCAGGGCCCAGATGGAGAACCTCTGCTAGGGCAGTGCGGAA
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GCATCAGCGTGACCCAGATGTGAGACATGGTGTCAAAGGAGATCATTTTGGAGCTTTAAG
                                                                     AGCCATACCCTGCAAAGCCACAGGGGGCAGAGTGGCCTGAGGCCATGGGAACCCACCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clones are available from Research Genetics (info@resgen.com). BAVend search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1998)
Other_GSSs: CIT-HSP-2337G10.TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lunalyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 623)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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301 838 0200
301 838 0208
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/note="Vector: pBeloBAC11; Site_1:
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/clone="2337G10"
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                tayggnaayccntggatgccnmgncaraarttygcngtnggngtnggnwsnwsntggmgn
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                                                               TATGGAAACACCTGGATGCCCAGGTAAAAGTTTGCTGCAGGGTGGAGGCCATCATGGAGA
                                                                                                                                   GCTGTGGCTTCAGAAGGTAGAAGCCCCAAGCCTTGGCAGCTTCCATGTGGTGTTGAGCCT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-AÜG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-85-93-9111, Fax:81-85-93-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG097258.1 GI:16717775
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-098001.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               677 bp DNA Pan troglodytes DNA, clone: PTB-098001.R, AG097258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Mammalia; Eutheria;
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R.Site 2
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                                                                                                                                                                                                                                                                                                       /clone="PTB-098001.R"
/sex="male"
/cell_type="lymphoblast"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
/clone_lib="PTB Chimpanzee Male
                                                                                                                                                                                                                                                                                                                                                                                                organism="Pan troglodytes"
/db_xref="taxon:9598"
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Primates;
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Human DNA sequence from GSSs, complete sequence. 282198 Z82198.2 GI:6572207 145880 bp DNA om clone RP1-302D9

Homo sapiens

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linear PRI 12-DEC-1999 chromosome 22 Contains

ALIGNMENTS

REFERENCE AUTHORS TITLE COMMENT JOURNAL Direct Submission

Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Dec 13, 1999 this sequence version replaced gi:3164067.

During sequence assembly data is comparred from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Bridgeman, A. (bases 1 to 145880) Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the entire insert
end of clone CTA-282F2 is at 69682
end of clone CTA-415G2 is at 55167
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/HGP/Chr22
RP1-302D9 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The following abbreviations are used to numbers given in the feature table with Em: EMBL; Sw: SWISSPROT: Tr: TREMBL; on the WORMPEP database can be found at
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                                                                                                                                                                    /note="52 copies 2 mer ct 78 conserved" 5181. .5491
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/note="Alusp repeat: matches 1.
1450. .1583
              /note="MADE1
7482. .7754
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                                                6988.
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/db_xref="taxon:9606"
                                              /note="AluSx repeat: 5988. .7036
                                                                                                                                                                                                                                                                               note="MLT1E repeat:
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3323. .3343
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                                                                                          note="MADE1 repeat: matches 1.
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repeat:
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                                                                                                                                                                                                                                                  matches 3.
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 matches
                                                           matches 1.
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8414...8551
/note="L2 repeat: matches 2553...
8914...9030
/note="MIR repeat: matches 147...
9110...9280
/note="MIR repeat: matches 91...2
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/note="MSTB repeat: matches 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat:
13806. .13919
/note="MIR repeat:
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16028. .16245
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/note="MIR repeat:
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13699. .13810
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13398. .13698
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13331. .13397
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10784. .11201
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/note="FAM repeat: matches 3.
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15669, .15727
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 /note="MSTA repeat:
18324. .18392
                                             note="AluY repeat: matches
                                                                             /note="MLT1B
                                                                                                                                                                                                     /note="MLT1B repeat: matches 1.
                                                                                                                                                                                                                                   'note="L2 repeat: matches 2112.
                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 49.
                                                                                                                                                                                                                                                                                                                               'note="match:
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23905. 23989
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18393. .18712
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19537. .20290
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1 (bases 1 to 154090)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J. Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
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COX.C., COyle, M.D., Dalling, S.K., David, M.D., Davy-Carroll, L.D., Dederich, D.A., Delaney, K.R., David, M.D., Delyado, O., Davy-Carroll, L.D., Delrich, H.A., Douthwaite, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Denn, A.C., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraqueo, D., Elhaj, C., Emerling, S., Escotto, M., Earls, T., Gabisi, A., Gao, J., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garrea, N., Gill, R., Gorrell, J.H., Guevara, W., Garrea, N., Gill, R., Gorrell, J.H., Guevara, W., Garrea, N., Gill, R., Gorrell, J.H., Guevara, W., Garrea, N., Han, J., Harris, C., Harris, K., Harris, K., Hand, J., Han, J., Harris, C., Harris, K., Harris, C., Harris, K., Harris, R., Hodgson, A., Holloway, C., Hollins, B., Homsi, F., Harris, K., Hand, J., Hand, J., Homsi, F., Hodgson, A., Holloway, C., Hollins, B., Homsi, F., Harris, K., Hand, J., Harris, R., Joudah, S., Harris, K., Holloway, C., Hollins, B., Homsi, F., Hodgson, A., Holloway, C., Hollins, B., Homsi, F., Hodgson, A., Holloway, C., Hollins, B., Homsi, F., Jackson, L., Kurah, J., Hodgson, R., Holloway, C., Hollins, B., Homsi, F., Hodgson, A., Holloway, C., Hollins, B., Homsi, F., Joudah, S., Warris, R., Homsi, F., Jackson, E., Kurah, J., Holloway, C., Hollins, B., Homsi, F., Jackson, L., Hodgson, A., Holloway, C., Hollins, B., Homsi, F., Jackson, L., Kurah, J., Holloway, C., Hollins, B., Homsi, F., Lee, E., Lewis, L.C., Expert, S., Homsi, F., March, R., Land, R., Land, R., Holloway, C., Hollins, B., Homsi, F., Wall, R., Wall, R., Martin, R., Wall, R., Wall, R., Martin, R., Wall, R., Holloway, J., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Chen,z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Unpublished Direct Submission (bases 1 to 154090)

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Worley, K.C.
Worley, K.C.
Direct Submission
Submitted (11-MAR-2000) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, USA

Worley, K.C.

REFERENCE TITLE

JOURNAL AUTHORS

Direct Submission
Direct Submission
Submitted (25-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 25, 2000 this sequence version replaced gi:9664948.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green

unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones an reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality a region does not meet this standard, it will be indicated in th annotation as Low Coverage. and 2

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

QUALSTAT-REPORT---

Number of N's in consensus :	Number of consensus changing edits:	Fraction of Phrap values less than 40 :	Average error rate (BCM-Phrap estimate):	Phrap values in estimate:	Contiq length:	Summary Statistics
C	22	0.0284086	0.000261755	153545	154090	

tantttttc(n)atctttaggg acctttagatg(n)ctcctccag cacagcttaa(n)caaggtaaga aaaaaagaa(n)gtaaggaaa acacaaaagaa(n)caaaacactc
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Distribution of Quality < 40 Bases

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Version: 1.01 Location/Qualifiers

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GAGGTCTTCATGGCAGCCCATCCCATCACAGGCCCGGAGGCCTAGGAGAAAATGGTTTTG
GTGCAAGCCCCAAGCCTTGGCAATTTCCATGTGTTGATGCCTGAGGGTGCACAGAAG 102112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAAGAAATTTCTAAGTAGCAAAGCATTAAAGAGGTGACTTAGATGTGGTTAAAGGTATT 101692
                                                                  CCAGCTGCTGCAGTGGTGGCTGAAAGGGGCCCAGCATAGAGCTTGGGCCGTGGCTTCGGAG
                   ggngcnwsnccnaarccntggcarytnccnwsnggngtngarccngtnggngcnaaraar 1188
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complement(6678..73:
/rpt_family="L1ME3"
7419..7454
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8666. .8695
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/chromosome="12"
/clone="RP11-13C3"
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MIZNY,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Dlng,Y., Dinh,H.H.,
Delaney,K.R., Delgado,O., Denn,A.L., Dlng,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C., Elhaj,C., Escotto,M.,
Earnhart,C., Edgar,D., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunardne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Holloway,C., Hollins,B.,
Hennandez,O., Hodgson,A., Hogues,M., Hume,J., Jackson,L.E.,
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Homo sapiens chromosome 12 clone RP11-307L1, WORKING
SEQUENCE, 1 unordered pieces.
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Mammalia; Eutheria; Pr
1 (bases 1 to 186660)
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Primates;
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Submitted (19-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 1, 2001 this sequence version replaced gi:13877175.
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                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Sequencing vector: M13;
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 18% of reads
Chemistry: Dye-terminator Big Dye: 82% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 18659 bases at least Q40
Consensus quality: 18659 bases at least Q30
Consensus quality: 18650 bases at least Q30
Consensus quality: 18650 bases at least Q30
Consensus quality: 18650 bases; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 10.7x in Q20 bases; sum-of-contigs estimation
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                                                                                                      Local Similarity
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On Jan 29, 2001 this sequence version replaced gi:12584354.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL: SW:. SWISSPROT: Tr:. TREMEL: Wp:. WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
http://www.sanger.ac.uk/Projects/Chr13
http://www.sanger.ac.uk/Projects/Chr13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RP11-279N8 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-279N8 is at 124518 in this sequence. The true left end of clone RP11-528D24 is at 114969 in this sequence. The true right end of clone RP11-214011 is at 100 this sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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VECTOR: pBACe3.6
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112388 .112496
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                                                                    28.5%; Score 493.6; DB 9;
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                                                                                                                                           ngcnytnmgnttygaytgyccnacnggnttymgnacntayatgggnccngtnccnytntg 1667
                                                                                                                                                                                           CCACCTCTTGCATCAGCATGACCTGGATGTGAGACATGGAGTCAAAGGAGATCATTTTGG
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                                                             TTTTGGCCAATTTCCCCCATTTGGAATGGGTATATTTACCCAATGCCTGTACCCCCATTG
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TITLE
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 116295 bases at least Q40 consensus quality: 121288 bases at least Q30 consensus quality: 122086 bases at least Q20 Estimated insert size: 123000; pulse field gel estimation Estimated insert size: 122770; sum-of-contigs estimation Quality coverage: 6.04 in Q20 bases; pulse field gel estimation Quality coverage: 6.05 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces to be contigned to be contigned to the pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens chromosome 5 clone CTD-2061E19, SEQUENCE, 8 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center Project Name: 651088
Center clone name: CITB-H1_2061E19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-AUG-1999) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459 on Jul 18, 2000 this sequence version replaced gi:7709316.
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DOE Joint Genome Institute
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DOE Joint Genome Institute.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                             37763
                                                                                                                                                                                                                           the accession number will be preserved.

1 9436: contig of 9436 bp in length
9437 9536: gap of unknown length
26538 26637: gap of unknown length
26538 46958: contig of 19321 bp in length
46959 68657: contig of 2259 bp in length
46059 68657: contig of 2259 bp in length
68658 68757: gap of unknown length
68658 68757: gap of unknown length
68658 68757: gap of unknown length
72152: contig of 3395 bp in length
72153 72252: gap of unknown length
72153 81169: contig of 8817 bp in length
81170 121547: contig of 40378 bp in length
121548 121647: gap of unknown length
121648 121647: gap of unknown length
12167070: contig of 40378 bp in length
121680 12167070: contig of 40378 bp in length
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                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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                                                                           /clone="CTD-2061E19"
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Best Local Similarity 46.7 Matches 495; Conservative
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ytngaygtnmgncayggngtnaarmgngaycayttyggngcnytnmgnttygaytgyccn 1629
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Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Vo. A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Vo. A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Vo. A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
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Vo. A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Vo. A., Wilson, B., Wu, X., Wy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 22, 2000 this sequence version replaced gi:7543856. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
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AC044889.2 GI:8016676
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        NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: 19594
Center clone name: 792_C_1
Center clone name: 792_C_1
Center clone name: 792_C_1
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 168749 bases at least Q40
Consensus quality: 180047 bases at least Q30
Consensus quality: 180047 bases at least Q20
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                                                                                                                                                                                                                                        Insert size: 190000; agarose-fp Insert size: 186268; sum-of-contigs Quality coverage: 3.8 in Q20 bases; Quality coverage: 3.9 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
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exact sizes of the
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COMMENT

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This record will be updated with the finished sequence as soon as it is available and the accession number wibe preserved.
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83451: contig of 4065
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92170: contig of 8619
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138021: gap of
157913: contig
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25287: contig of 2703 l
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1092: contig of 5726 bp in
2: gap of 100 bp
5262: contig of 4070 bp in
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1069: contig of 2885 bp in
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51: contig of 1934 bp in
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p of 100 bp
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                                       wsnathcargargtnacntgggtnytnytnaargcnttywsnttyathmgngargcngar 825
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18628. 20561
/note="assembly_fragment"
20662. 22484
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22585. 25287
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9795. 11004
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25388. .27603
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13008. .14916
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2385. .3898
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1116. .2284
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/clone_lib="RPCI-11 Human Male
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/db_xref="taxon:9606"
/chromosome="2"
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45367. .51092
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27704. .30020
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17215. .18527
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11105. .12907
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55363. .60982
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51193. .55262
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Pred. No. 2.7e-109;
20; Mismatches 309;
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                                     Homo sapiens chromosome 4 clone SEQUENCE, 4 unordered pieces. AC017063
                        AC017063
AC017063.7 GI:16596637
             HTG; HTGS_PHASE1;
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86475 CATAAAAGTCTGGAAAATTTGCAGTCCGACAATGTGATAAGAAAAGAAAATTCCATTTTCT
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                                                                                        conconwsnwsnmgnythodaraarggnmgnwsnacngaywsnythodardaygthodngar
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HTGS\_DRAFT; HTGS\_ACTIVEFIN

DNA linear RP11-354H17, WORKI

WORKING

HTG 02-NOV-2001 DRAFT

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JOURNAL
REFERENCE
AUTHORS
                                                BASE COUNT
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 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-primer ET; 34% of reads Chemistry: Dye-terminator Big Dye; 66% of reads Assembly program: Phrap; version 0,990319 Consensus quality: 197437 bases at least Q30 Consensus quality: 198145 bases at least Q30 Consensus quality: 198648 bases at least Q20 Consensus quality: 198648 bases at least Q20 Insert size: 200000; agarose-fp Insert size: 200801; sum-of-contigs Quality coverage: 10.58 in Q20 bases; sum-of-contigs Quality coverage: 10.55 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson_wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.H.

Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Nov 2, 2001 this sequence version replaced gi:15741601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1
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Mammalia; Eutheria; Primates;
1 (bases 1 to 198545)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number be preserved.
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NOV 2, 2001 this sequence version replaced g1:15741601
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5053. .198545
                                                                                                                                                           /note="assembly_name:Contig38" 2817. .4952
                                                                                                                                                                                           /note="
1275. :
                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
                                                                                                        /note="assembly_name:Contig44
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1. .198545
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1274: gap of unknown length
2716: contig of 1442 bp in length
2816: gap of unknown length
4952: contig of 2136 bp in length
5052: gap of unknown length
198545: contig of 193493 bp in length
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Best Local Similarity 47.0 Matches 498; Conservative
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                                                                                                                                                                                                                                                                                                                           Sequencing vector: plasmid; 10%
Chemistry: Dye-primer ET; 81% of reads
Chemistry: Dye-terminator Big Dye; 19% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 144558 bases at least Q40
Consensus quality: 149743 bases at least Q30
Consensus quality: 152625 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 18975; sum-of-contigs
Quality coverage: 3.48 in Q20 bases; sgarose-fp
Quality coverage: 3.75 in Q20 bases; sum-of-contigs
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Submitted (07-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jul 7, 2000 this sequence version replaced gi:7801489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACU35233 161575 bp DNA linear HTG 07 Homo sapiens chromosome 17 clone RP11-333E1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; 90%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: H_NH0333E01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Center code: WUGSC
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Waterston, R.H.
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1. (bases 1 to 161575)
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AC025233.4 GI:8954317
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                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                       preserved.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Verteb
Mammalia; Eutheria; Primates; Catarrhini; Homi
I (bases 1 to 163674)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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AC087500.4 GI:18104839
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                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 17, clone RP11-333E1
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* 79597 79696: gap of 100 bp

* 79697 86804: contig of 7108 bp in length

* 86805 86904: gap of 100 bp

* 86905 133464: contig of 36560 bp in length

* 123465 123564: gap of 100 bp

123565 160329: contig of 700 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (05-JAN-2001) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Jan 10, 2002 this sequence version replaced 91:13560412. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                             44782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34527 60200: contig of 5574 bp in length 60201 60300: gap of 100 bp 60301 70374: contig of 10074 bp in length 70375 70474: gap of 100 hm 70475 79506.
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3135 3234: gap of 100 bp
3235 27783: contig of 24549 bp in length
27784 27883: gap of 100 bp
27884 50218: contig of 22335 bp in length
50219 50318: gap of 100 bp
50319 54526: contig of 2335 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
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50319 54526: contig of 4208 bp in length
54527 54626: gap of 100 bp
                                                                                                                                                       /clone="RP11-333E1"
/clone_lib="RPCI-11 Human
37406 c 35496 g 44882
                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Score 488.8; DB 2;
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Homo sapiens SEQUENCE, 31 AC015727
                      175639 bp DNA linear chromosome 17 clone RP11-420A6 map 17, unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on sep 9, 2000 this sequence version replaced gi:6958075.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1 (bases 1 to 175639)
Birren,B., Linton,L.,
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HTG; HTGS_PHASE1; HTGS_I
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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NOTE: This is a 'working draft' sequence. It currently consists of 31 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
13947; contig of 13947 bp in length
13948 14047; gap of 100 bp
14048 14259; contig of 212 bp in length
14260 14359; gap of 100 bp
14360 14359; gap of 100 bp
153040 15139; gap of 100 bp
15140 15139; gap of 100 bp
15833 15932; gap of 100 bp
15833 15932; gap of 100 bp
1689; contig of 693 bp in length
1690 16789; gap of 100 bp
1693 18192; gap of 100 bp
1699 16790 16790 pp in length
18093 18192; gap of 100 bp
18093 18192; gap of 100 bp
18093 18192; gap of 100 bp
18093 18193; contig of 1303 bp in length
                                                                                                                                                                                                                                                                                                                be preserved
                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L1423
Center clone name: 420_A_6
Center clone name: 420_A_6
Center clone name: 420_A_6
Sequencing vector: M13; M77815; 87% of reads
Sequencing vector: Plasmid; n/a; 13% of read
Sequencing vector: Plasmid; n/a; 13% of read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye; 96% of rea Assembly program: Phrap; version 0.960731 Consensus quality: 161512 bases at least 040 consensus quality: 167866 bases at least 030 consensus quality: 170654 bases at least 020 consensus quality: 170654 bases at least 020 Insert size: 17000; agarose-fp Insert size: 172639; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-primer-amersham; 4% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
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.960731
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20093: gap of 22205: con

23915: ~

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81789 81888: gap of 100 bp 86379: contig of 4491 bp in length 86380 86479: gap of 100 bp 86380 86479: gap of 100 bp 1548 91547: contig of 5068 bp in length 91548 91647: gap of 100 bp 91783: contig of 6136 bp in length 91784 97883: gap of 100 bp 105190: contig of 7307 bp in length 105191 105290: gap of 100 bp 111855: contig of 6565 bp in length 111856 111955: gap of 100 bp 111956 119820: contig of 7865 bp in length 1119821 119920: gap of 100 bp 111956 119820: contig of 7865 bp in length 119821 119920: gap of 100 bp 
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33116 35727: contig of 2612 bp in length
35728 35827: gap of 100 bp
35828 59255: contig of 23428 bp in length
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77528 81788: contig of 4261 bp in
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                                                                                                                                       /note="assembly_fragment"
15933. .16689
                                                                                                                                                                                  /clone="RP11-420A6"
/clone_1ib="RPCI-11 Human
1. .13947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                     note="assembly_fragment"
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18193. .19993
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16790. .18092
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11379; contig of 11379 bp
131399; gap of 100 to
139546; conti
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30454: contig of 1503 bp in
554: gap of 100 bp
33015: contig of 2461 bp in
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77427: contig of 4153 bp in length
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26544: contig of 2529
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                                   Center: Sanger Centre
                                                                                             requests: clonerequest@sanger.ac.uk
On Dec 28, 2000 this sequence versi
                                                                                                                                                         Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgesh CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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HTG; HTGS_PHASE1; HTGS_CANCELLED
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                                                                      ----- Genome Center
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Insert size: 162786; 7.7% error; agarose-fp
Quality coverage: 4.40x in Q20 bases; sum-o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: bA319F1
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Contact: humquery@sanger.ac.uk
----- Project Informatio
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88689 94602: contig of 5914 bp in length
94603 94702: gap of 100 bp
94703 105410: contig of 10708 bp in length
105411 105510: gap of 100 bp
105511 107644: contig of 2134 bp in length
107645 107744; gap of 100 bp
107745 126586: contig of 18842 bp in length
126587 126686: gap of 100 bp
125587 126686: gap of 100 bp
155611 155710: gap of 100 bp
155711 173103: contig of 17393 bp in length
173204 173203: gap of 100 bp
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8897 8996: gap of 100 bp
8997 22635: contig of 13639 bp in length
22636 22735: gap of 100 bp
22736 55625: contig of 32890 bp in length
55626 55725: gap of 100 bp
55726 65440: contig of 9715 bp in length
65441 68540: gap of 100 bp
65541 8858: contig of 23048 bp in length
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100 bp

173203: contig of 17393 bp

173203: gap of jon'

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                                               CAGTGCAGAAGGAAAATGTGGGGGTCAGAGCCCCCACCACAGAGTCCCTACTGGGGCACCAC
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                   source
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                                                                                                                                       Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 13% of reads Chemistry
Dye-terminator Big Dye; 86% of reads
Consensus quality: 76604 bases at least Q40
Consensus quality: 77098 bases at least Q40
Consensus quality: 77320 bases at least Q20
Insert size: 7405; sum-of-contigs
Insert size: 85298; 1.5% error; agarose-fp
Ouality coverage: 4.54x in Q20 bases; sum-of-contigs
Coverage: 4.30x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
                                                                                                                                                                                                                                                                                                                                                Center project name: bA435A2
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Aug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL353634 77405 bp DNA linear HTG 10-JUL-2001 Homo sapiens chromosome X clone RP11-435A2 map q21.33-22.3, *** SEQUENCING IN PROGRESS'***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Sanger Centre
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HTG; HTGS_PHASE2; HTGS_CANCELLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                   NOTE: This is a 'working draft' sequence. This sequence will be replaced by the finished sequence as soon as it is the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21, 2000 this sequence version
                     Location/Qualifiers
1. .77405
/organism="Homo sapiens"
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                                                                                                                                TGGAAGGGAAAAGTGGGGTCATAGCCGCCACACAGAGTCCCTACCAGGGGGACCACCTAGT
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                                                CTGCACCGTGTGCCTGGAAAAGCCGCAGACACTCAATGCCAGCCTGTGAAAGCAGCAGGG
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/chromosome="x"
/map="q21.33-22.3"
/clone="RP11-435A2"
/clone_11b="RPCI-11.2"
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14551 c 15133 g 22649 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on Jul 29, 1999 this sequence version replaced g1:5566565. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence is the entire insert of clone 633H17. This sequence has been finished according to sequence map criteria as follows. A base been finished according to sequence map criteria as follows. A
                                                                                                                                                                                                                                                                                                                                            Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Informatic on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/HGP/Chr1
633H17 is from the library RPCI-4 constructed at the Roswell Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was generated from part of bacterial clone human chromosome 1, constructed by the Sanger Centre Chromapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moore, M.
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oxidase; glutamic-oxaloacetic transaminase; GOT2; MTATP8; MTCO1;
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(bases 1 to 1245
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/map="p31.2-32.2"
/clone_lib="RPCI-4"
                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                  /chromosome-"1"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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124531)
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complement(235. .546)
/note="match: GSS: Em:AQ055811"
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/note="HERVL repeat: matches 4676. .5241 of consensus"
                                                                        /note="MER5A repeat: 21201. .21331
                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 28. .169 of consensus"
20273. .20334
/note="1TR16C repeat: matches 90. .152 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 7..107 of consensus"
18377. .18492
/note="MER39b repeat: matches 476. .574 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="23 copies 2 mer tt 74% conserved"
18053. .18154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match: GSS:
complement(16459.
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14656. .14764
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/note="L1MA
                                       /note="MER5A repeat: matches 56.
21466. .21528
                                                                                                                           /note="18 copies 2 mer ac 94% conserved"
                                                                                                                                                              note="L2 repeat: matches 2660. .2693 of
                                                                                                                                                                                   20692
                                                                                                                                                                                                /note="LTR16C repeat: matches 190. .376 of consensus"
                                                                                                                                                                                                                                   /note="MER81
                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 10.
19866. .20007
                                                                                                                                                                                                                                                                                                                                                             l8525. .18954
/note="match: GSS: Em:AQ210513"
l9026. .19126
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|6531...16576
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|6410. .17037
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16403. .16945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note-"match: GSS: Em:B30406"
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/note="L2 repeat: matches 2349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L2 repeat: matches 2389.
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10623. .10689
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                                                                                                                                                                               . .20725
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                                                                                                                                                                                                                                  repeat:
                    repeat: matches 214. .285 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Em: AQ309712"
.16861)
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                                                                                       matches
                                                                                       40.
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                                                      .188 of consensus
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/notce-"HERVL repeat: matches 3020. .3235 of consensus"
30122. .30487
/notce-"MLT1A2 repeat: matches 1. .374 of consensus"
30488. .30578
/notce-"HERVL repeat: matches 2933. .3020 of consensus"
                                                                                                                                            /note="MIR repeat: matches 20. .129 of consensus"
34831 .35552
                                                                                                                                                                                                                                                                                                                                                             33175. .33412
/note="L2 repeat: matches 2473.
33454. .33885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="HERVL repeat: matches 1792. .2933 of consensus"
complement(31888. .32090)
/note="match: GSS: Em:B58153; match: GSS: Em:B66544;
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/note="MER93
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26898. .27373
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22864. .23010
/note="L2 repeat: matches 2329.
23011. .23310
/note="Alubb repeat: matches 1.
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22394. .22748
/note="MLT1B repeat: matches 1.
22749. .22846
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22083. .22259
                                                                                                                                                                                                      34303 .34334

/note="MIR repeat: matches 129.

34335 .34703
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33896. .33946
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/note="match: GSS: Em:AQ127976"
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/note="12 repeat: matches 2585. .2692 of consensus" 25745. .25785
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23433. .23730
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22280. .22393
                                                                                       note="L2 repeat: matches 2675.
                                                                                                                       note="L1MC2 repeat: matches 5573. .6325
                                                                                                                                                                                              note="THE1C repeat: matches 1.
                                                                                                                                                                                                                                                                     note="THE1B repeat: matches 1.
                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 162.
                                                                                                                                                                                                                                                                                                                                                                                                             32922. .33453
/note="match: GSS: Em:AQ751315"
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27912. .28051
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23731. .25397
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 28.2%;
                                     L2 repeat: matches 2638.
.37648
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 Score 488.2;
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                                                      .2707 of consensus"
                                                                                       .2723
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269722.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-FEB-1995) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquires: humpub@sanger.ac.uk IMPORTANT: This sequence is the entire insert of clone U212C1. true left end of clone U212C1 is at 1 in this sequence. The truright end of clone U212C1 is at 40714. U212C1 is from the human chromosome X-specific cosmid library.
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smmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 40714)
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16204. 16495
/note="Alu repeat: matches 1. . . 16532. . 16609
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932. .1108
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2571. 2617
/note="MER43 element fragment"
2613. .5203
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14824. .15044
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16073. .16149
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16651. .16712
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16626. .16737
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16624. .16722
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16026. .16155
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15421. .15849
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15234. .15369
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/clone="LL0XNC01-212C1"
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/db_xref="taxon:9606"
/chromosome="X"
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40640. .40693
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32232. .32735
/note="MER9 element fragment"
35168. .35654
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/note="MSTC element fragment"
27949. .28241
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22661. .22730
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19720. .19797
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/note="THE1B element
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/note="THR element fragment"
24643. .25270
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23725. .24279
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23550. .23697
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20518. .20734
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20007. .20256
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/note-"THE1B_element fragment"
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ACCESSION VERSION

Homo sapiens genomic DNA, complete sequence. AP004219 AP004219.2 GI:18146615

KEYWORDS

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, Hayashi K, Saito K, su A, Nagai K, Otsuki T			NO:11697. diagnosis; antisense therapy;	ВР.	ALIGNMENTS	AAHU 3678 AAHU 3678 AAAS91984 AAAS919984 AAAS91262 AABA21079 AAI99255 AAI63605 AAK70266 AAK70266 AAK70266 AAK70266 AAK70266 AAK70266 AAK70266 AAK70267 AAK70267 AAK70267 AAK70267 AAK70267 AAK70267 AAK70267 AAK70267 AAK70321 AAAG4678 AAK70321 AAAG4678 AAK70321 AAAG4678 AAS40321 AAAG4678 AAS40321 AAAG4678 AAAG4678 AAAG4678 AAAG4678 AAAG4678 AAAG4689 AAK8046623 AAK804679
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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
  ID 11697;
2537pp +
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  ROM;
  English
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The present invention describes primer sets for synthesising 5602 (C full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of c the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the c complementary strand of a polynucleotide which comprises a 5'-end c sequence and an oligonucleotide comprising a sequence complementary to a combination of c polynucleotide which comprises a 3'-end sequence, where the coligonucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 1 least 15 nucleotides and the combination of c the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and c in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the combination of c detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cC AAH13633 to AAH13672 represent human amino acid sequences; AAB9246 to AAH13620 c AAH13629 to AAH13632 c of the present oligonucleotides, all of which are used in the exemplification of the present oligonucleotides, all of which are used in the exemplification. present invention.

Sequence 2590 B₽; 722 A; 526 Ç 670 <u>ი</u> 672 Τ; 0 other;

Match Local Similarity

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Conservative

293; Indels 22;

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negative; blood group typing; blood transfusion; ant
ic disease of the newborn; chromosome 1 p34.1-p36; ds
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                                   99EP-0121686
2000EP-0111696
                                                                      2000WO-EP10745
                                                                                                                                                                 /note= "Binding site of complement (3034..3054)
                                                                                                                                                                                                    Location/Qualifiers 32..54
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CR HHD gene deletion in Rh negative haplotypes. The Rhesus genes

CR iocus comprises the RHD, SMP1 and RHCE (ail undefined) genes and/or the

CR clocus comprises the RHD, SMP1 and RHCE (ail undefined) genes and/or the

CR Rhesus box(es), preferably the hybrid Rhesus box, the upstream Rhesus box

CR Rhesus box(es), preferably the hybrid Rhesus box, the upstream Rhesus box

CR Rhesus box(es), preferably the hybrid RHCE genes are located at

CR chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the

CR HHD deletion in the common RHD negative haplotypes. The sequence has

CR been used to design primers which are useful for: (1) the specific

CR detection of the common RHD positive haplotypes in D-negative

CR cl individuals; (2) blood group typing; (3) determining whether a patient

CR can be transfused with RhD negative blood and whether blood is suitable

CR for transfusion to patients who should not be exposed to antigen C; (4)

CR assessing the risk of a RhD negative mother of conceiving or carrying an

CR RHD positive foetus. Anti-D antibodies are useful for treating pregnant

CR women who are Rhesus D negative, where the foetus is not homozygous for

CR the RHD gene to treat or prevent haemolytic disease of the newborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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47.48;
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Pred. No. 2.4e-105;
2; Mismatches 282;
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31-MAY-2000;
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                       Disciosure; Fig 9; 135pp; Engiish.
                                                                                                              (DRKB-) DRK
                                                                                                                                                         31-OCT-2000; 2000WO-EP10745
                                                                                                                                                                           10-MAY-2001.
                                                                                                                                                                                             WO200132702-A2
                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                               Rhesus box; RHD positive; sequence iength polymorphism; SSP; RHCE; Rh negative; blood group typing; blood transfusion; ant haemolytic disease of the newborn; chromosome 1 p34.1-p36; ds
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                                       nucleic acid molecular structure, useful for detection of common positive haplotypes in D-negative individuals, comprises RHD, SM RHCE genes -
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1 p34.1-p36; ds.
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The sequence represents the coding sequence of Rhesus gene upstream Rhesus box of D positives. The Rhesus genes locus  $\frac{1}{2} \frac{1}{2} \frac{1}{2$ 

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comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the Rhesus box(es), preferably the hybrid Rhesus box, the upstream Rhesus box and/or the downstream Rhesus box. The RHD and RHCE genes are located at chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the RHD deletion in the common RHD negative haplotypes. The sequence has been used to design primers which are useful for: (1) the specific detection of the common RHD positive haplotypes in D-negative haplotypes. Individuals; (2) blood group typing; (3) determining whether a patient can be transfused with RHD negative blood and whether blood is suitable for transfusion to patients who should not be exposed to antigen C; (4) assessing the risk of a RhD negative mother of conceiving or carrying an RhD positive foetus. Anti-D antibodies are useful for treating pregnant women who are Rhesus D negative, where the foetus is not homozygous for the RHD gene to treat or prevent haemolytic disease of the newborn.
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Sequence 9236 BP; 2467 A; 2319 C; 2000 G; 2450 T; 0 other;

Length 9236;

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Pred. No. 6.3e-105;
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                                                                              GAGCTTTAAGATTTGACTGCCCCACTGGATTTTGGACTCTCATGGGCCTGTAGCCTCTTT
                                                                                                            standard; DNA; 9236
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29-AUG-2001

Rhesus gene locus: downstream Rhesus box of D-positives

Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; RHCE; Rh negative; blood group typing; blood transfusion; antigen haemolytic disease of the newborn; chromosome 1 p34.1-p36; ds. Ç

Homo sapiens.

WO200132702-A2

10-MAY-2001

31-OCT-2000; 2000WO-EP10745

02-NOV-1999; 31-MAY-2000; 99EP-0121686 2000EP-0111696

(DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG

WPI; 2001-291052/30

RHD nucleic acid molecular positive haplotypes in RHCE genes structure, D-negative useful for detection individuals, comprise comprises RHD, of common SMP1

Disclosure; Fig 10; 135pp; English

The sequence represents the coding sequence of Rhesus gene locus:

downstream Rhesus box of D positives. The Rhesus genes locus
comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the
comprises the RHD, SMP1 and RHCE genes and/or the
Rhesus box(es), preferably the hybrid Rhesus box, the upstream Rhesus box
and/or the downstream Rhesus box. The RHD and RHCE genes are located at
chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the
RHD deletion in the common RHD negative haplotypes. The sequence has
been used to design primers which are useful for: (1) the specific
detection of the common RHD positive haplotypes in D-negative
individuals; (2) blood group typing; (3) determining whether a patient
can be transfused with RhD negative blood and whether blood is suitable
for transfusion to patients who should not be exposed to antigen C; (4)
assessing the risk of a RhD negative mother of conceiving or carrying an
RHD positive foetus. Anti-D antibodies are useful for treating pregnant

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Best Local Similarity
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             cnggnatggarwsngtnccntayaaracngtngtngcngarytnacnaaracngtnggna
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                                                     CCCACCCTTCCATCTGCGTGACCTGGATGTGAGATGTGGAGTCAAAGGAGATCATTTTG
                                                                 GGATGCCCAGTCAGAAGTTTGCTGCAGGAGCAGGGCCCTCATGGAGATCCTCTGCCAGGG
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Pred. No. 6.3e-105;
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Query Match Best Local s Matches 485

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                                                                                                    The sequence represents the coding sequence of Rhesus gene locus:

Chybrid Rhesus box of RHD negatives. The Rhesus genes locus

comprises the RHD, SMP1 and RHCE (all undefined) genes and/or the

Comprises the RHD, SMP1 and RHCE (all undefined) genes are located at the common stream Rhesus box. The RHD and RHCE genes are located at chromosome 1 p34.1-p36. Rhesus box. The RHD and RHCE genes are located at chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the RHD deletion in the common RHD negative haplotypes. The sequence has been used to design primers which are useful for: (1) the specific detection of the common RHD positive haplotypes in D-negative individuals; (2) blood group typing; (3) determining whether a patient can be transfused with RhD negative blood and whether blood is suitable for transfusion to patients who should not be exposed to antigen C; (4) assessing the risk of a RhD negative mother of conceiving or carrying an RhD positive foetus. Anti-D antibodies are useful for treating pregnant when who are Rhesus D negative, where the foetus is not homozygous for the negative blood and whether blood spreaments as the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the foetus is not homozygous for the negative where the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 8; 135pp; English.
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and
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31-MAY-2000;
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therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 24 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system disorder; AIDS; autoimmune disease; rheumatoid ari inflammation; allergy; neurological disorder; Alzheimer's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy; binding partner identification; ss.
gastrointestinal disorders, pregnancy related disorders, disorders, and infections. The proteins can also be used healing and epithelial cell proliferation, to prevent sk
                                                 AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, cardiovascular disorders, angiogenic disorders, kidney disorders, and cardiovascular disorders (e.g., and cardiovascular disorders).
                                                                                                                                                                                                                                                The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or therapy. Pathological conditions can be diagnosed by determining
                                                                                                                                                                                                                                                                                                     AAD05121-AAD05203 represent cDNAs corresponding to 24 human secreted protein genes, and AAE01232-AAE01311 represent the proteins they encode. AAE01312-AAE01340 represent human secreted protein variants or fragments
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              tgccnmgncaraarttygcngtnggngtnggnwsnwsntggmgnacnwsngcnmgngtng
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nccnccnwsnwsnmgnytncaraarggnmgnwsnacngaywsnytncarcaygtnccnga
                                                           gtaggagcccccacacagagtccctactgg-gcaccacttggtggagctgttagaagaga
                                                                            ntgggarccnccncaymgngtnccnwsnggngcnccnwsnwsnmgngcngtnmgnmgnws
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207; Mismatches 303;
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RESULT 10
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XX AAL036
XX Human;
XW Human;
XW Human;
XW Cancer
XX Homo 9
XX Hom
   31-JAN-2000
04-FEB-2000
24-FEB-2000
16-MAR-2000
11-MAR-2000
11-MAR-2000
11-MAY-2000
07-JUN-2000
07-JUL-2000
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 2000US-0179065.
2000US-018638.
2000US-0184644.
2000US-018464.
2000US-019874.
2000US-0198123.
2000US-0214886.
2000US-0211687.
2000US-0211687.
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2000US-0211687.
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03-NOV-2000
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Best Local Similarity 46.4%; P
Matches 475; Conservative 210;
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17-NOV-2000
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                                                      cDNA sequence
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Human; primer;

detection;

diagnosis;

antisense therapy;

gene therapy;

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EP1074617-A2

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Best Loc
Matches
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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Ishii
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Sugiyama
                                                                                                                                                                                                                                                                                                                                                       1736
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakamatsu
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Pred. No. 1.1e-97;
1; Mismatches 293;
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A, Nagai K,
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                               Human; oestrogen receptor alpha; ESR-alpha; ER; chromosome 6; Synaptic nucle1 expressed gene 2; haplotype; cytostatic; osteopar cardiant; vasotrople; gene therapy; vaccine; cancer; osteoporosicardiovascular disease; oestrogen receptor; ds.
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20-OCT-2000; 2
24-JAN-2001; 2
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; 2000US-0692414.
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46.5%; Pr
vative 213;
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food supplement; medical imaging; diagnostic; genetic
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(HYSE-) HYSEQ INC
                       31-MAR-2000;
23-AUG-2000;
                                                            30-MAR-2001; 2001WO-US08631
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                        2000US-0540217
2000US-0649167
                                                                                                                                                                                                  novel human diagnostic protein #27788
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CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cc at fip.wipo.int/pub/published_pct_sequences.
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Best Local Similarity
Matches 458; Conser
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           congtnggngcnaaraarw8nmgnathgargtntgggarconconathmgnttycaraar
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cctgtgggtgcacagaagtcaagaactgaggtttgggaacctctgcctagatttcagaag
                                               tgggctgtggcttcagagggtgcaagacccaagccttggcagcttccacgtgatgttgag
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                                                                                                          Location/Qualifiers 224..268
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immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; sathma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferative disorders, cancer, tumours, feetal and developmental abnormalities, haematopoietic disorders, diseases of the immune syst. AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, cardiovascular disorders, angiogenic disorders, kidney disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD05121-AAD05203 represent cDNAs corresponding to 24 human secreted protein genes, and AAE01232-AAE01311 represent the proteins they encode. AAE01312-AAE01340 represent human secreted protein variants or fragments
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aggtcttcatggcagcccctcccatcacagaccctgaagactaggaggaaaaaatggttt
                                            mgnwsnwsncarcarwsnathaarwsnytngcntggmgnccnmgnmgnaar---tggtty
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                                                                                                                                                      DNA encoding
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2000US-0540217
2000US-0649167
                                                                                                                   mapping; gene mapping; gene therapy; medical imaging; diagnostic; genetic
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Local Similarity 42.4%; Pred. No. 2.6e-92;
Les 466; Conservative 215; Mismatches 383;
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                                                                                                                                                                                                                                                                    2001-639362/73.
DB; ABG23075.
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                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1449 raarwsnacngayacncartgycarccngtnaargcngcnggnatggarwsngtnccnta 1508
                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
APPLICATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                      CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nathmgnttycaraarathtayggnaayccntggatgccnmgncaraarttygcngtngg 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaaagccacagacactcaacaccagcctgtgaaggcagctggaagggaggctgtaccctg 48051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyggnacngcngtnttyacncartgyytntayytncaytgyat 1730
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                                                                                                                                                                                                                                         350 Cambridge Avenue,
                                                                                                                                                                                       USA
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                                                                        Version
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Best Local :
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TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                       14736 TGCCTAGTGGAGCTGTGAGAAGACAGCCACTGTCCTCCAGACTGGTAGATCCCCCCAGAAT 14677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14794
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14378
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                                                                                                                                  14498
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
                                 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
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hes 221; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        congtnaargongonggnatggarwsngtnoontayaaracngtngtngongarytnaon 1533
                    yytntayytncaytgyat 1730
                                                                                ccngt-nccnytntgyttyggncarttyttyccnttyggnacngcngtnttyacncartg 1712
                                                                                                                               GAGATCATTCTGGAGCTTTAAGATACACCTGCCCCACTGAATTTCGGACTTGCACGGGG
                                                                                                                                                    mgngaycayttyggngcnytnmgnttygaytgyccnacnggnttymgnacntayatgggn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGCAATATGGAAGGGAAATGTGGGGGTTGAAACCCCCAC--AGAGTTCCTATGGAGGGGAC 14737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGTATCCCCATTGTAT 14361
                                                                CCTGTAGCCCCTTTGTTTTGGCCAATTTCTCCCATTTGGAATGGCTGTATTTGCCCAATG
                                                                                                                                                                                                     AAGGCCATGGAAGCCCACCTCTTGCATCAGAGTGACCTGGATGTGAGACATGGAGTCAAA
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                                                                                                                                                                                                                                                                                                                                      AATAGATCCACTGACAGCTTGCACTGTGCACCTGGAAAAACTGCAGGCACTCAACACCAG
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Pred. No. 2.2e-39;
90; Mismatches 172;
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WESULA US-08-991-789A-29 ; Sequence 29, Application US/08991789A ; Patent No. 6225054 ; PATENT INFORMATION: ; APPLICANT: Frudakis, Tony N. ; Reed, Steven G.

TITLE

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TOPOLOGY: Tinear
SEQUENCE DESCRIPTION: SEQ ID
US-08-991-789A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                II26 garggngcnwsnccnaarccntggcarytnccnwsnggngtngarccngtnggngcnaar II85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1299
1594 mgngaycayttyggngcnytnmgntt----ygaytgyccnacnggnttymgnacntayat 1649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1239 naayccntggatgccnmgncaraarttygcngtnggngtnggnwsnwsntggmgnacnws 1298
                                                                                                                                                                                                                                                                                                                                                     243
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                                                                                                                                                                                                                                                     303
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #I.0, Vers
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/991,789A
FILING DATE: I1-Dec-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME. Detro: 140.0 P
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Seed IF
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                                                                                                                                                                                                                                                                                                                                                                            ngcnccnwsnwsnmgngcngtnmgnmgnwsnccnccnwsnwsnmgnytncaraarggnmg I4I8
                                                                                                                                                                                                                                                                                                                                                                                                                                          aarwsnmgnathgargtntgggarccnccnathmgnttycaraarathtaygg----- 1238
|||::: ||:||: | ||:|| ||
                                                                                               aracngtnggnathtayytnytncaytgycaygayytngayg-tnmgncayggngtnaar I593
                                                                                                                                                                                                                                                                            nwsnacngaywsnytncarcayg-tnccngaraarwsnacngayacncartgycarcc-- I475
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                                                                                                                                                                                                                                                                                                                                                  AACACTGCCTAATGAAACTGTGAGAAGATGGCCACTGTCATCCAGACACCAGAATGATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAACACCTAGATATTCAGACAAAAGTTTACTACAGGGATGAAGCTTTCACGGAAAACCTC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGGTACCAGCCCCAAGCCTTGACAACTTCCATAGGGTGTCAAGCCTGTGGGTGCACAG 62
                                                                                                                                                                          -ngtnaargcngcnggnatggarwsngtnccntayaaracngtngtngcngarytnacna 1534
                                                                                                                                                                                                                                                ACCCACCAAAAACTTATGCCATATTGCCTATAAAACCTACAGACACTCAATGCCAGCCCC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTCAAAAATTGAGTTTTGGGATCCTCAGCCTAGATTTCAGAGGATATAAAGAAACACC 122
                                                                                                                                                   ATGAAAAAAAACTGAGAAGAAGACTGTNCCCTACAATGCCACCGGAGCAGAACTGCCCC 422
                                                   AGGCCATGGAAGCACAGCTCTTATATCAATGTGACCTGGATGTTGAGACATGGAATCCNA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative IO5; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EE: Seed IP Law Group
70I Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%; Score 164.6; DB 4; 40.7%; Pred. No. 4.3e-37;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-49
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Frudakis, Tony I
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
1299 ngcnmgngtngtncaraarggnaaygtnggntgggarccnccncaymgngtnccnwsngg I358
                                                                                                                                                                     II86 aarwsnmgnathgargtntgggarccnccnathmgnttycaraarathtaygg----- 1238
                                                                                                                                                                                                                                                  II26 garggngcnwsnccnaarccntggcarytnccnwsnggngtngarccngtnggngcnaar II85
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APPLICATION NUMBER: US/0
FILING DATE: 04-APR-I997
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAS: NUMBER OF SEQUENCES: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I709 artgyytntayytnc I723
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                                                              123 TAACACCTAGATATTCAGACAAAAGTTTACTACAGGGATGAAGCTTTCACGGAAAACCTC 182
                                                                                                                                                                                                                                                                                                          y Match 9.5%; Score I64.6; DB 4; Length 620;
Local Similarity 40.7%; Pred. No. 4.3e-37;
hes 250; Conservative I05; Mismatches 243; Indels I7
                                                                                                                                             63 AAGTCAAAAATTGAGTTTTGGGATCCTCAGCCTAGATTTCAGAGGATATAAAGAAACACC I22
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #I.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 620 base pairs
                                                                                                                                                                                                                           g-ggnccngtnccnytntgyttyggncarttyttyccnttyggnacngcngtnttyacnc I708
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                                                                                 naayccntggatgccnmgncaraarttygcngtnggngtnggnwsnwsntggmgnacnws I298
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GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAM.
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAM.
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-128-155-16
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                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 324; Conserv
                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 16
LENGTH: 152331
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C
-09-128-155-16
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naarttyaarytngcngcngarathtgyathtgyaaygargarytnaaygtnaayccnca
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                                                  Conservative 168;
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                                                                                                                                                                                               Score 140.6; DB Pred. No. 1e-27; 8; Mismatches 4
                                                                                                                                                                                                                                     DB 3;
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RESULT 6 US-08-687-080-59

Sequence 59, Application Patent No. 5965427 GENERAL INFORMATION:

US/08687080

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: APPLICANT: Gregory Dolganov

Human 175

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Methods

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ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Avenue, Sui

Suite

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STATE: C. COUNTRY: CITY: Palo Alto

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                                                    caytgycaygayytngaygtnmgncayggngtnaarmgngaycayttyggngcnytnmgn 1617
ttttttttttggtcacaggtgtttgaac 72195
                ttyttyccnttyggnacngcngtnttyac 1706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS: LENGTH: 14855 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 01 FILING DATE: 26-JAN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           798 rgcnttywsnttyathmgngargcngarcayaarwsnwsngaraayytncayccngayaa 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sholtz, Charles REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/687,080 FILING DATE: 17-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
tng
                                                           thmgnttycaraarathtayggnaayccntggatgccnmgncaraarttygcngtnggng 1276
                                                                                                                                                                                                                  CATTTCAGAGATCTTCACAGCAGCCCCTCCCATTACAGGACACTACTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    yathtgyaaygargarytnaayg-tnaayccncargayaayggngaraayathwsntgga 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ygtnathaaraaraayccnttywsngarggnaarttyaarytngcngcngarathtg 917
                                  CTAGATTTCAGGGGATGTATGGAAACGTCTGGATGTCCAGGCAGAAGTCTGCAGGACTTG 5636
                                                                                                                                    cnwsnggngtngarccngtnggngcnaaraarwsnmgnathgargtntgggarccnccna 1216
                                                                                                                                                                                                                                                                                                           ggttytgyggnacnggnccnggnwsnytntgytgygtncarccnmgngayytngtnccnt 1096
                                                                                                                                                                                                                                                                                                                                                                                       cntgycarmgnwsnwsncarcarwsnathaarwsnytngcntggmgnccnmgnmgnaart 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                CATAAGTAAAGAGGAGCAGAATGTTTAATAGCCAAGACACTGGGGAAAATGGCTAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTGGTAGAAAAGAAAAACCCATTTTCTGGGGAGGAATTCAAGCCGGCTGCAGAAATTTG 5306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAACTTATATTTAAAAGGGAAGCAGAGCATAAAAGTTTGGAAAATTTGCACCCTGATCA 5246
                                                                                                                  CACATGGTGTTAAGCCTGGGGTTGCGCAGAGAACAAGAGTTGAGGCTTGGGAAGCCTCCAC
                                                                                                                                                                                                                                                                       TGTGTTTCAGCCACTCCAGCTCCAGCCATGGCTAAAAGGGCCCCCAGATATATC-----
                                                                                                                                                                                           -----TTAAGCTGCTGCTCCAGAGGCTGCAAGCTGTAAGCCTTGGCAGCTTC 5516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
  1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.8%; Score 135.8; DB 2; ilarity 39.5%; Pred. No. 2.2e-27; Conservative 101; Mismatches 160;
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Best Local 9
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                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                1416
1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE
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                                                                                               700
                                                                                                                                                         640 ttygcntgymgngtnccnggnaaytaytaywsnwsnttygaygtngarytncaycaytgy 699
                                                                                                                                                                                                                         580 athathttyacnggngtnytntayaaygcncarmgngayytnaargargcnatgggngtn 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE TEAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                              aargtnaayathtggytnatgmgnaarcarathytngcnaayaargargarathwsnaar 759
                            carcarwsnathcargargtnacntgggtnytnytnaargcnttywsnttyathmgngar 819
                                                              ATCGCTTCTAGACGCATCTATTCAGTTTCAAAAAACGGCATGTAGGCATCACTGTAATTA 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14, Application US/08232463
5. 5670367
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                                                                                                                                                                                                                                                                         h 3.9%; Score 67; DB 1;
Similarity 12.6%; Pred. No. 5.7e-08;
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                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                             203;
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                                                                                                                                                                                                                                                                                       Length 7218;
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US-09-106-194-11
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                Query Match
Best Local Similarity
Matches 101; Conserv
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                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: ZPPAR4
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 206-442-6674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1201 EXCITY: Seattle STATE: WA COUNTRY: USA ZIP: 98102
                                                                                                                                                                                                                               LENGTH:
TYPE: 1
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Leith, Debra K REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/106,194
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                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                       2067 base pairs
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Durnam, Diane
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                                                                                                                                                                                                                                                                                                                                                                 206-442-6678
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                     Conservative 297;
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SYSTEM: DOS
                                                                                                                                                                              linear
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                                      3.48;
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                Score 59; DB 4;
Pred. No. 3.1e-06;
97; Mismatches 67
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                                              ATHWSNAAYGGNYTNWSNAAYYTNAAYAAYGARACNWSNGGNACNTAYGCNAAYGGNCAY
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                                                                                            cngaraarwsnacngayacncartgycarccngtnaargcngcnggnatggarwsngtnc 1504
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US-08-463-911-6
RESULT 10
US-09-140-804-9
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI9;
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 861-6240
TELECAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 75; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C
STREET: Two Militia Drive
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MOLECULE TYPE:
                                                                           572 ATATGAAGGATGTGAAGGTCAGCCTCTTCAAGAAGGACA
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LOCATION:
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CITY: Lexington
STATE: Massachu
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STRANDEDNESS: single
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34.2%; Pred. No. 0.00022;
7ative 36; Mismatches 108;
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US-09-053-866-3/c; Sequence 3, Application US/09053866; Patent No. 611075; GENERAL INFORMATION:
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SEQ ID NO 9
LENGTH: 4517
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
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                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,866
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
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EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
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CURRENT FILING DATE: 1998-08-26
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PROTEASE-ACTIVATED RECEPTOR TITLE OF INVENTION: PAR4 (ZCHEMR2)
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632 tgggngtnttygcntgymgngtnccnggnaaytaytaywsnwsnttygaygtngarytnc 691
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                                                                                                                                                                                                                                                                               STATE: V
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CITY: S
                                                                                                                                                                                                                                                                 ZIP: 98102
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: ZymoGenetics, Inc. STREET: 1201 Eastlake Avenue
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                                                                                                                                                                                                                                                                                                                       Seattle
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Yee, David P.
Foster, Donald C.
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LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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REGISTRATION NUMBER: 32,619
REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6674
  1436
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Local Similarity 6.3%; Pred. No. 0.00043;
hes 64; Conservative 256; Mismatches 703; Indels 0
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arcaygtnccngaraarwsnacngayacncartgycarccngtnaargcngcnggnatgg
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                                                                                                                                                                                arggnaaygtnggntgggarccnccncaymgngtnccnwsnggngcnccnwsnwsnmgng 1375
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                                             RTTCATNARNARCATNGTNSWNGGNARNCKNGGNGCYTGNGTNGCNARNACCCANARNGC
                                                                                                                                       NARRTGRTANGCDATNCKNGGNGGNARNGCNARNGCNARNARRARTCNGCNGTNGCNAR
                                                                                                                                                                                                                                  RTANARNGCNGCNGTNGCNARNCKRCANGCNGCYTCNCCRAANGGCCANCKYTGNCCNCK 412
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                                                                                      cngtnmgnmgnwsnccnccnwsnwsnmgnytncaraarggnmgnwsnacngaywsnytnc
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; OTHER INFORMATION: This degenerate OTHER INFORMATION: sequence of SEQ NAME/KEY: misc_feature LOCATION: (1)...(2082) OTHER INFORMATION: n = A,T,C or G US-09-440-325A-2
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US-09-440-325A-2
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TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09440325A
Patent No. 6280994
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/440,325A
CURRENT FILING DATE: 1999-11-15
NUMBER OF SEQ ID NOS: 3
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acnttygarcaytaygtngarytnwsnaayaargcngcncarytnaayggngtnnnnaar
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                                      snytngcntggmgnccnmgnmgnaartggttytgyggnacnggnccnggnwsnytntgyt 1069
                                                                                    gargarytnytntgggcntggcarggntggcargaygcngtnggnmgncarathtgyacn
                                                                                                                             argayaayggngaraayathwsntggacntgycarmgnwsnwsncarcarwsnathaarw 1009
                                                                                                                                                                         garggnccntgyytnwsnytngarwsngarytngargtnatggcnacnwsnmgngayaar
                                                                                                                                                                                                                    gnaarttyaarytngcngcngarathtgyathtgyaaygargarytnaaygtnaayccnc
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82; Conserv
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ilarity 10.4%;
Conservative 19
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1%; Pred. No. 0.0026;
191; Mismatches 512;
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GENERAL INFORMATION:
APPLICANT: Baindur, Nand
APPLICANT: Baindur, Nand
APPLICANT: Baindur, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT FILING DATE: 199-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2088
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                  ; NAME/KEY: misc_feature; LOCATION: (1)...(2088); OTHER INFORMATION: n = A,T,C US-09-351-414-3
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US-09-351-414-3
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Matches 140; Conserv
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LOCATION: (1)...(2088)
OTHER INFORMATION: n is any
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EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
GENERAL INFORMATION:
APPLICANT: SZOSTAK, Jack W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SUSLECTION OF PF
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/2
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US-09-007-005-17
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; Sequence 17, Application US/09244796

; Patent No. 6281344
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Best Local :
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APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
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CURRENT FILING DATE: 1998-01-14
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LOCATION: (1)...(289)
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ORGANISM: Artificial Sequence
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CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: 60/035,963

EARLIER FILING DATE: 1997-01-27

EARLIER APPLICATION NUMBER: 60/064,491

EARLIER FILING DATE: 1997-11-06

EARLIER APPLICATION NUMBER: 09/007,005

EARLIER APPLICATION NUMBER: 09/007,005

EARLIER FILING DATE: 1998-01-14

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FRASTSEQ for Windows Version 4.0

SEQ ID NO 17
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TYPE: RNA
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ALIGNMENTS

## REFERENCE AUTHORS TITLE JOURNAL COMMENT KEYWORDS SOURCE ACCESSION VERSION RESULT BE420422 밁 S BASE COUNT ORIGIN FEATURES Source LOCUS DEFINITION Matches Query Match Best Local Similarity ORGANISM 706 494 aayathtggytnatgmgnaarcarathytngcnaayaargargargarathwsnaarcarcar 765 ||: |: |:| |:| || || || ||: AACCTTGAGCTTGAGAGAGATCATTTAGGGTATCTGGCAGAAAATTTCTAAGCAGCAA 553 500; Lu,X., Cui,L. and Li,Y. DDRT-PCR from B cell Unpublished (2000) Contact: xingwu Lu,liangxian Cui,yonghai Li Department of Biochemistry Institute of Basic Medical Science, Peking Union Medical College DongDan SanTiao 5, Beijing, P.R.C, 100005 Tel: 86-010-65296951 Fmail. 10:10-65296951 sequence. BE420422 BE420422.1 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Email: luxingwu@263.net full-length and coding sequence. fucation/Qualifiers 1..2615 32-393 human bone marrow Mammalia; Eutheria; 1 (bases 1 to 2615) EST human. 705 Conservative ď /organism="Homo sapiens" /db\_xref="taxon:9606" /clone\_lib="human bone marrow /tissue\_type="bone marrow" 531 c 641 g 738 t GI:16041640 27.7%; Score 479.2; DB 10; 47.1%; Pred. No. 2.6e-99; tive 222; Mismatches 299; 2615 bp mRNA linear EST 11-OC; CDNA library Homo sapiens CDNA, mRNA cDNA library" Indels Length 2615; 41; EST 11-OCT-2001 Gaps 4;

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Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greene, Mark Ketteman and Anuradha Madan
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Anup Madan, Rachel Dickhoff, Jessica Fahey,
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Contact: MGC help desk
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/Tab_host="DH1DB-R"
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                                                               Lu,X., Cui,L. and Li,Y.

DDRT-PCR from B cell

Unpublished (2000)

Contact: xingwu Lu,liangxian Cui,yonghai Li
Department of Biochemistry

Institute of Basic Medical Science, Peking Uni
DongDan SanTiao 5, Beijing, P.R.C, 100005

Tel: 86-010-65296951
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Similarity 47.1%; Pred. No. 1.1e-80;
27; Conservative 182; Mismatches 256
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/db_xref="taxon:9606"
/db_sref="taxon:9606"
/clone_lib="human B lymphocyte
/tissue_type="bone marrow"
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                                               GAGGAAAAAGAGGTTTCGTGGGCCAGGCCCAGCATCCCCGTGCTTTGTGCAGCCTAGGGA 241
                                                                nmgnmgnaartggttytgyggnacnggnccnggnwsnytntgytgygtncarccnmgnga 1085
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11479 row: k column: 04
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Eukaryota; Metazoa; Chordata; Craniata; verue
Eukaryota; Metazoa; Chordata; Craniata; verue
Catarrhini; Hominidae;
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BI488505.1 GI:15327733
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603021014F1 NIH_MGC_114
mRNA_sequence.
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National Institutes of Health, Mammalian
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/db_xref="taxon:9606"
/clone="IMAGE:5191803"
/clone=1ib="NIH_MGC_114"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                            Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-d7 primed and directionally cloned (sorv site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
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AGENCOURT_6465359 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5539381
5', mRNA sequence.
BM472108
                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 1050)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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                                                                   CDNA Library Preparation: Life Technologies, Inc. CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM1233 row: m column: 14
                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
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                                    quality sequence stop: |
| Location/Qualifiers
/organism="Homo sapiens"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sall; Cloned unidirectionally. Onstructed by Life Average insert size 2 kb. Library constructed by Life Technologies."
Technologies. 272 g 221 t
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Email: cgapbs-r@mail.nih.gor
Tissue Procurement: ATCC/DCTD/DTP
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Consortium (LLNL)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA)
Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM1293 row: g column: 18
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BM471183
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1 (bases 1 to 1036)

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Nath MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                     sntggmgnacnwsngcnmgngtngtncaraarggnaaygtnggntgggarccnccncaym 1345
                                                                    araarathtayggnaaycontggatgccnmgncaraarttygcngtnggngtnggnwsnw 1285
                                              AGAAGATGTATGGAAATGCCTGGATGCCCAGGCAAAAGTTTGCTGCAAGGTTGGGGCCCCT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.6%; Score 321.8; DB 10;
h similarity 45.0%; pred. No. 3.4e-63;
SO; Conservative 166; Mismatches 267;
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/
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo. Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo. National Institutes of Health, Mammalian Gene Collection (MGC) Rational Institutes of Health, Mammalian Gene Collection (MGC) Contact; Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be http://lnage.linl.gov
High quality sequence start: 9
High quality sequence start: 9
High quality sequence start: 9
LCCation/Qualifiers
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AG086951 717 bp DNA
Pan troglodytes DNA, clone: PTB-085H08.F,
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GSS 03-NOV-2001 urvey sequence

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SOURCE ORGANISM ACCESSION VERSION KEYWORDS

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DEFINITION

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BAC end sequences of Library PTB
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AG086951.1 GI:16638753
GSS; GSS (genome Survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
Pan troglodytes male lymphoblast
Pan troglodytes male lymphoblast
BAC Library clone:PTB-085H08.F.
BAC Library clone:PTB-085H08.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); apan and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 17-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mali-chimpbesdegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/. Tenali-chimpbesdegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/. Tel.81-45-503-9111, Fax:81-45-503-9170) This BAC end Tel:81-45-503-9111, Fax:81-45-503-9170) This BAC end Clones are derived from the chimpanzee BAC library pTB This BAC end clones are derived during the R&D process and may have higher chance of was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujlyama A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T. Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
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                                                                                                                                                                                   GGGGGCTCATGAAAAACCTCTGCTAGGGCAGTGTGGGAGAAAATGTGGGGGTCAGAGCC
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                                                  ATCACACAGAGTCCCTACTGGGGCACCGCCTAGTGGAGCTGTGAAAAGTGGGCCACTATT 388
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ngayacncartgycarcongtnaargongonggnatggarwsngtncontayaaracngt 1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.1%; Score 313; DB 12;
illarity 49.1%; pred. No. 2.8e-61;
Conservative 113; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pan troglodytes"
/db_xref="taxon:9598"
/cione="pTB-085H08.F"
/sex="maie"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ceil_type="lymphoblast"
/clone_lib="pTB Chimpanzee Maie BAC Library"
/clone_lib="pTB Chimpanzee Maie BAC Library"
189 c 195 g 158 t
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694 TGGTCTGGACCCAAGGTCCCCATGTTGTGTGCAGCCTAGGACTTGCTGCCTTGTGTCCCA 635
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B1754555 736 bp mRNA clone IMAGE:5194028 5',
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Tissue procurement: Life Technologies, Inc.
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Edurary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
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Contact: Robert Strausberg, Ph.D.
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found through the I.M.A.G.E. Consortium/LLNL at:
fitte://image.lln.gov
plate: LLAM11485 row: g column: 21
plate: LLAM11485 row: g column: 21
High quality sequence.scop: 733.
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_2: EccRV (destroyed); RNA source anonymous pool of 6
Site_2: EccRV (destroyed); RNA source anonymous pool of 6
Site_2: EccRV (destroyed); RNA source anonymous pool of 6
Site_2: EccRV (destroyed); Library 2 you Library 1: destroyed primed and directionally cioned (EccRV Site 1: destroyed primed and directionally ciones is ze 1: kb. Insert size primed and cioning). Library 1: normalized and enriched for range 1:3 kb. Library 1: normalized by C. Gruber range 1:3 kb. Ciones and was constructed by C. Gruber full-length ciones and was constr
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9666"
/db_xref="inAGE:5194028"
/cione_inb="NIH_MGC_114"
/lab_host="DH10B"
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                                                                                                                                              122;
                                                                                                                                           Score 306.6; DB 1
pred. No. 8.8e-60;
2; Mismatches 266
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1673 gncarttyttyccnttyggnacngcngtnttyac 1706
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          Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Torumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@Sc.riken-go.jp, URL:http://hgp.gsc.riken.go.jp/
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                               GGCCATTTCTCCCATTTGGAATGGCCGTATTCAC 1
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                                                                                            Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
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Pan troglodytes DNA, clone: PTB-119B01.R, genomic survey sequence.
AG112666.1 GT:16733185
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
Pan troglodytes
Pan troglodytes
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                                                                                                                                                Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end seguences of Library PTB
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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COMMENT

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ACCESSION VERSION KEYWORDS SOURCE

DEFINITION RESULT 10 AG112666 LOCUS

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                                                                                                                                        CCTGTAGCCCCTTAGTTATGGCCAATCTCCCCATTTGGAATGGCTGCACTTCACCCATG
                                                                                                                                                                                                                                              AAGACTAGGGGAACCTACCTCTTGCATCAGCATGACCTGGATGTGAGGCACGGAATCAAG
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AG064424 676 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-053H24.R, genomic survey seguence
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/clone="PTB-119801.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
a 174 c 180 g 135 t
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AG064424.1 GI:16616226
GSS; GSS (genome survey sequence).
GSS; GSS (genome male lymphoblast DNA, clone_lib:PTB Chimpanzee Male pan troglodytes male lymphoblast DNA, clone_lib:PTB-053H24.R.
BAC Library clone:PTB-053H24.R.
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pirect Submission _____
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/cell_type="rptB Chimpanzee Male BAC Library"
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JOURNAL
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ORIGIN
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Best Local S
                                                                                  Matches
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A0062447.1 GI:16614249
A0062447.1 GI:16614249
A0062447.1 GI:16614249
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Mule
Pan troglodytes male 1978-050M20.F.
BAC Library clone:PTB-050M20.F.
Pan troglodytes
Pan troglodytes
Figure Morance. Charders. Cranists. Vartabrats. Fiitalagetomi:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission

Olevander 2001) Asao Fujlyama, The Institute of Physical Submitted (02-Aug-2001) Asao Fujlyama, The Institute of Physical Submitted (02-Aug-2001) Asao Fujlyama, Sciences Center (GSC); Submitted (02-Aug-2001), Genomic Sciences Center 230-045, Japan and Chemical Research (RIKEN), Genomic Sciences 230-045, Japan and Chemical Research (Northern 20-1p), URL:http://hgp.gsc.riken.go.jp/
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
(E-mail:chimpbes@gsc.riken.go.jp.)

(E-mail:chimpbes@gsc.riken.go.jp.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 691)
Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                         cal similarity
301, Conserv
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R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vector
                                                                                                                                                                                                                          /organism="pan troglodytes"
/db_xref="taxon:9598"
/clone="prB-050N20.F"
/cetx="male"
/sex="male"
/cell_type="lymphoblast"
/clone_lb="prB Chimpanzee Male BAC Library"
/clone_lb="prB Chimpanzee Male BAC Library"
/clone_lb="prB Chimpanzee Male BAC Library"
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: SacI
                                                                                                   16.6%; Score 287.4; DB 12; Length 691; 49.0%; pred. NO. 2.3e-55; tive 110; Mismatches 196; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                           : Sacı
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1458 ngayacncartgycarccngtnaargcngcnggnatggarwsngtnccntayaaracngt 1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1338 nocncaymgngtnocnwsnggngcnocnwsnwsnmgngcngtnmgnmgnwsnocnconws 1397
                                                   Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 CCCACACAGAGTCCCTACTGGGGCACCACCAGTGGAGCTGTGAGAAGAGGGGCCACTGTC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1278 nggnwsnwsntggmgnacnwsngcnmgngtngtncaraarggnaaygtnggntgggarcc 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1218 hmgnttycaraarathtayggnaayocntggatgccnmgncaraarttygcngtnggngt 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 AGGGCCCTCATGGAGAACTTCTGCTAGGGCAGTGTGGAAGGGAAATGTGAGGTCAGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 TAGATTTCAGAAGATGTATGAAAATACCTGGATGCCCATGCAAAAGTTTGCTGTAGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 ATGTGGTGTTGAGCCTGTGAGTGCACAGAAGA-----ATCGGGGTTTGGGAACCTCCACT 196
                                                                                                                                                                     2 (bases 1 to 720)
Pujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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AG116938
AG116938
AG116938
AG116938
AG116938.1 GI:16737457
GSS: GSS (genome survey sequence).
BAC Library clone:pTB-124K01.R.
Pan troglodytes male lymphoblast DNA, clone_1ib:PTB Chimpanzee Male_pan troglodytes
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Source
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                                                                                                                                                               647 CCTGTAGCCCTTTTGTTTTGGCCAATTTCTCCCCATTTGGAATGGTTGCATTTACCTAATG 706
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Best Local Similarity 48.5%; Score 286.2; DB 12; Length
Matches 298; Conservative 112; Mismatches 200; Indels
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                                                                                                                                                                                                                                                                              527 GÁGACCATGGGAÁCCTÁCCTCTTGCÁTCAGGGTGÁCCTGGÁTGTGAGACATGGATTCAAA 586
                                                                                                                                                                                                                                                                                                                                      467 CCCATGAAAGCAGCTGGGAGGGAGGCTGTACCCTGCAAAGCAACAGAGGTGGAGCTTCCC 526
                                                                                                                                                                                                                                                                                                                                                                                                               1414 ggnmgnwsnacngaywsnytncarcaygtnocngaraarwsnacngayacncartgycar 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409 GCTAGATCCACTGACACTTGC--ACCTGTGCCTGGAAAAGCTGCAGGTACTCAACATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 ACTGGGG-ATCACCTAGTGGAGGTGTGAGAGAGACAGCGACTGTCTTCCAGACCCCAGAAT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 ACCTCTGCTAGGGCAGTGCAGAAGGGAAATGTGGGGTCGGAGCCCCCACACAGGGTCCCT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1174 gtnggngcnaaraarwsnmgnathgargtntgggarccnccnathmgnttycaraarath 1233
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                                                                                                                                   TCTGTATTCCCATT 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 GCCATGGCTTCAGATGGTGCAAGCAGCCAAGTCTTGGTGGCTTCCACATGGCATTGAGCCT 169
AQ037711 623 bp DNA linear GSS 11-JUL-1998 sequence. AQ037711 GI:3303543
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/Clone="PTB-124KDLR"
/Sex="male"
/cell_type="lymphoblast"
/Clone_lib="pTB-Chimpanzee Male BAC Library"
31 a 186 c 187 g 165 t 1 others
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COMMENT

Sequencing: M13Rev

TITLE JOURNAL REFERENCE AUTHORS

Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB

TITLE JOURNAL

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE DEFINITION ACCESSION

ORGANISM

Eukaryota;

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Best Local Similarity 48.1%; Pred. No. 1.3e-Ja,
Matches 286; Conservative 111; Mismatches 196; Indels
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                                                                                                                                                                    rcaygtnccngaraarwsnacngayacncartgycarccngtnaargcngcnggnatgga 1496
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                                                                       AGCCATACCCTGCAAAGCCACAGGGGCCAGAGTGGCCTGAGGCCATGGGAACCCACCTCTT
                                                                                                  rwsngtnccntayaaracngtngtngcngarytnacnaaracngtnggnathtayytnyt 1556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams,M.D., Rounsley,S.D., Zhao,S., Fleld,C.E., Bass,S., Linher,K. Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
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Other_GSSs: CIT-HSP-2337G10.TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mdadams@tigr org
Clones are available from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Building (1998)
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301 838 0208
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HindIII"
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/clone="2337Gl0"
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.9o.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee
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BAC Library clone:PTB-098001.R.
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Fujiyama, A., Hattori, M.,
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Mammalia; Eutheria;
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/db_xref="taxon:9598"
/clone="PTB-098001.R"
/sex="male"
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/clone_lib="PTB Chimpanzee Male
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